



SEQUENCE LISTING



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Oomen, Raymond P.

<120> Identification of Polynucleotides
Encoding Novel Helicobacter Polypeptides in the Helicobacter
Genome

<130> 06132/041002

<140> US 09/881,752

<141> 2001-06-15

<150> US 08/833,457

<151> 1997-04-01

<160> 370

<170> FastSEQ for Windows Version 4.0

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<211> 265

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(212)

<400> 1

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                                     Met Glu
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ttt ttg gga ctg att tta agt ctg gcc gct att ttg ata gcg ttt aaa      104
Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys
      5              10              15

aag cct gaa aaa gaa aat tgg gcg ttt ggg att ttg atg gtg gtg tgg      152
Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp
      20              25              30

tta gtg gag ctt att att ttt ata gcc cac agc tct agc gtt ttg cct      200
Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro
      35              40              45              50

aac atg aat cta taagggggat gcatggataa agaaacccga ttttacaacc      252
Asn Met Asn Leu

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ttttttctttt ggc

265

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<212> PRT

<213> Helicobacter pylori

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		20					25					30			
Val	Trp	Leu	Val	Glu	Leu	Ile	Ile	Phe	Ile	Ala	His	Ser	Ser	Ser	Val
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Leu	Pro	Asn	Met	Asn	Leu										
	50														

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<213> Helicobacter pylori

<220>

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<222> (51)...(617)

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aaa	att	gct	ttc	att	ttg	gct	104
Lys	Ile	Ala	Phe	Ile	Leu	Ala	
	5				10		
						15	
gag	cct	aaa	aaa	agt	cat	att	152
Glu	Pro	Lys	Lys	Ser	His	Ile	
	20				25		
						30	
cct	att	aaa	ata	acc	cca	aaa	200
Pro	Ile	Lys	Ile	Thr	Pro	Lys	
	35				40		
						45	
						50	
ttt	tta	tgg	ggg	gct	aaa	gga	248
Phe	Leu	Trp	Gly	Ala	Lys	Gly	
			55			60	
						65	
cta	gcg	tta	agg	ggg	gaa	ttt	296
Leu	Ala	Leu	Arg	Gly	Glu	Phe	
		70				75	
						80	
gca	ctg	cac	acg	att	aac	act	344
Ala	Leu	His	Thr	Ile	Asn	Thr	
	85					90	
						95	

tta agc gat ttt tac act tac aaa aaa tac agc ttt ggg gtg tat ggg 392
 Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly
 100 105 110

 ggg ctt ggg ata ggg tat ttt tat caa agc aac cat tta ggc atg aaa 440
 Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys
 115 120 125 130

 aat agt tcg ttt atg ggt tat aac ggc ttg ttt aat gtg ggg ctt ggc 488
 Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly
 135 140 145

 agc acg atc gat cgc cac cac cgc ata gag ctt ggg gct aaa atc cct 536
 Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro
 150 155 160

 ttt tca aag act aga aat tct ttt aaa aat cct tat ttt tta gag agc 584
 Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser
 165 170 175

 gtt ttt atc cat gcg act tat agc tat atg ttt taagagagaa tagcctatta 637
 Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe
 180 185

gtggtcgtta tcaataagat aagatcctta atg 670

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 <212> PRT
 <213> *Helicobacter pylori*

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 Leu Ala Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr
 35 40 45
 Thr Ala Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe
 50 55 60
 Lys Ala Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys
 65 70 75 80
 Pro Thr Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile
 85 90 95
 Asp Val Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val
 100 105 110
 Tyr Gly Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly
 115 120 125
 Met Lys Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly
 130 135 140
 Leu Gly Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys
 145 150 155 160
 Ile Pro Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu
 165 170 175

Glu Ser Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe
180 185

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<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(380)

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Met Leu
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aaa aaa agt ttg tta ttg ctt gtt ttt tta gtc tta cag ctt agc ggc 104
Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly
5 10 15

gct gaa gaa aac aat caa gcc cca aaa aac acg ccc cct gaa tta aac 152
Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn
20 25 30

ccc gct aac gct aag ggc gcg cca aac tct aac acc cag atc acc cct 200
Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro
35 40 45 50

aaa aac gat aac tct aac ctg tta gac aaa tta ggt tcg cct gaa aac 248
Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn
55 60 65

gct caa acc gag ctt tct gcc ggt att gat ttg gct aaa aag ggc gat 296
Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp
70 75 80

tat caa ggg gct ttc aag ctt ttt tcc caa tcg tgc gat aat ggt aat 344
Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn
85 90 95

gcg gcc ggg tgt ttt gca agt ggg ggc gat gta tgc taatggggta 390
Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
100 105 110

gggatccaaa ccaacagatt aaaagccgct cgctattatg aatg 434

<210> 6
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<212> PRT
<213> Helicobacter pylori

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1				5					10					15			
Ser	Gly	Ala	Glu	Glu	Asn	Asn	Gln	Ala	Pro	Lys	Asn	Thr	Pro	Pro	Glu		
			20					25					30				
Leu	Asn	Pro	Ala	Asn	Ala	Lys	Gly	Ala	Pro	Asn	Ser	Asn	Thr	Gln	Ile		
		35					40					45					
Thr	Pro	Lys	Asn	Asp	Asn	Ser	Asn	Leu	Leu	Asp	Lys	Leu	Gly	Ser	Pro		
	50				55					60							
Glu	Asn	Ala	Gln	Thr	Glu	Leu	Ser	Ala	Gly	Ile	Asp	Leu	Ala	Lys	Lys		
65				70				75						80			
Gly	Asp	Tyr	Gln	Gly	Ala	Phe	Lys	Leu	Phe	Ser	Gln	Ser	Cys	Asp	Asn		
			85					90					95				
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 <213> Helicobacter pylori

<220>
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 <222> (73)...(522)

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 Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser
 1 5 10

gct cac ctc tct aaa atc att ctt ttt tta aac acc ggc ttt tta gcc 159
 Ala His Leu Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala
 15 20 25

tat ctg tta agc gct tgt ggg gcg aat gtg cct ata gaa gaa gtg ttg 207
 Tyr Leu Leu Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu
 30 35 40 45

ggt aaa gat cct aaa gag acc aaa gcc caa gaa gtc gcc aga gaa gaa 255
 Val Lys Asp Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu
 50 55 60

aag gct atc cag caa gaa aac gcc act att gat gcg cgc acc acg cct 303
 Lys Ala Ile Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro
 65 70 75

tta atc aat cgt ttc act aat tat agc gct tat ggc tct tta aac ggc 351
 Leu Ile Asn Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly
 80 85 90

ttt tac aat tca gtg gat aat ctc aat tcg ccc atg caa aac ggg atg 399
 Phe Tyr Asn Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met
 95 100 105

tat gga ggc tat tac atg cct tat tat tac atg ccc tat ggt ttc atg 447

Tyr Gly Gly Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met
 110 115 120 125
 cct tat ggg tca ggt ctt atg cct tat ggg cct tat ggg tat gga gcg 495
 Pro Tyr Gly Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala
 130 135 140
 cct gga tac ttc cct tac gct ttt tat tgattgagtg gcttttagaaa 542
 Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr
 145 150
 gcgtggtggt gttggtgttt ttactcaaac acg 575

<210> 8
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 <212> PRT
 <213> Helicobacter pylori

<400> 8
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 Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu Val Lys Asp
 35 40 45
 Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu Lys Ala Ile
 50 55 60
 Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro Leu Ile Asn
 65 70 75 80
 Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly Phe Tyr Asn
 85 90 95
 Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met Tyr Gly Gly
 100 105 110
 Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met Pro Tyr Gly
 115 120 125
 Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala Pro Gly Tyr
 130 135 140
 Phe Pro Tyr Ala Phe Tyr
 145 150

<210> 9
 <211> 910
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(860)

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Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu Gly Asn	
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agt ctt gtg gca gca gaa ggc agc aca gaa gtg caa aag caa ttg gaa	152
Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln Leu Glu	
20 25 30	
aag cca aaa gag tat aaa gca gtg aaa ggc gag aaa aac gct tgg tat	200
Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala Trp Tyr	
35 40 45 50	
ttg ggg att agc tat caa gtc ggt cag gct tcg caa agc gtt aaa aac	248
Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val Lys Asn	
55 60 65	
ccc ccc aaa agc agt gaa ttt aac tac cct aag ttc cct gtg ggt aaa	296
Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val Gly Lys	
70 75 80	
acc gac tat ctg gcc gtt atg caa ggc tta ggg ctt act gtg ggt tat	344
Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val Gly Tyr	
85 90 95	
aag cag ttt ttc ggg gaa aag aga tgg ttt ggt gca cgc tat tac ggc	392
Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr Tyr Gly	
100 105 110	
ttc atg gat tat ggg cat gcc gta ttt gga gcg aac gct tta aca tcg	440
Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu Thr Ser	
115 120 125 130	
gat aat ggt ggg gtg tgt gag ctt cac caa cca tgt gcg acc aaa gta	488
Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr Lys Val	
135 140 145	
ggg aca atg ggc aat ctg tct gac atg ttc act tat ggt gtg ggt att	536
Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val Gly Ile	
150 155 160	
gac act tta tac aat gtc atc aat aaa gaa gat gcg agt ttt ggt ttc	584
Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe Gly Phe	
165 170 175	
ttt ttt ggg gct caa atc gcg ggt aac tct tgg ggt aat acg aca ggg	632
Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr Thr Gly	
180 185 190	
gcc ttt ttg gaa act aaa agc cct tat aag cac act tcc tat agc ctt	680
Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr Ser Leu	
195 200 205 210	
gat ccg gcg att ttc cag ttc ctt ttt aat tta ggg atc cgc acc cat	728
Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His	
215 220 225	

att ggc cgg cat caa gaa ttt gac ttt ggc gtg aag att ccc act atc 776
 Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile
 230 235 240

aat gtt tat tat ttt aac cat ggg aat ttg agc ttc act tac cgc cgt 824
 Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg
 245 250 255

caa tac agc ctt tat gtg ggg tat cgt tac aat ttc tgatttaaaa 870
 Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
 260 265 270

cgcttgtttt tctctaattg aattttcaat tagagttttc 910

<210> 10
 <211> 270
 <212> PRT
 <213> Helicobacter pylori

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 20 25 30
 Leu Glu Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala
 35 40 45
 Trp Tyr Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val
 50 55 60
 Lys Asn Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val
 65 70 75 80
 Gly Lys Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val
 85 90 95
 Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr
 100 105 110
 Tyr Gly Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu
 115 120 125
 Thr Ser Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr
 130 135 140
 Lys Val Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val
 145 150 155 160
 Gly Ile Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe
 165 170 175
 Gly Phe Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr
 180 185 190
 Thr Gly Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr
 195 200 205
 Ser Leu Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg
 210 215 220
 Thr His Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro
 225 230 235 240
 Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr
 245 250 255
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 260 265 270

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (58)...(1305)

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 Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile
51015

ttt ttt tta aat ggt ctg tct ttg aaa gct tta gaa atc gcc gtc aaa 156
 Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys
202530

cct ttt ggc tat ctg ggg cta tta tat aat caa ggg gcg caa aaa aac 204
 Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn
354045

cct cac agc tat gtg ggg gct tta gcg cgt ctt ggg gtg gat ttt tct 252
 Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser
50556065

tat agc aac ggg tgg tcc ttt ggt att gga gcg att ggg gct tgg aat 300
 Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn
707580

att tat aac aaa cag cgt ttg gct aac ctt tat atc agt cta ggg aat 348
 Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn
859095

ttt ttt ggt agt tct aaa aat gtt aaa cct tat ttg agc gct ggc gat 396
 Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp
100105110

gtt tct gat gcg tat gtt caa tac act aac cag cgt ttt aaa atc gct 444
 Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala
115120125

tta ggg cgt ttc aat acc gat ttt gtg gat ttt gat tgg ata ggg ggc 492
 Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly
130135140145

aat att caa ggg gtt tct gta gct ttt aag caa aat tcc atg cgt tat 540
 Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr
150155160

ttt ggg att ttt atg gat agc atg ctt tat aat ggg cat caa atc aac	588
Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn	
165 170 175	
aaa gag caa ggg aat cgg atc gct act tcc cta aac gct cta gcg tct	636
Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser	
180 185 190	
tat gac cct gtg tct aaa cgc ttg tat gtg ggg ggg gaa gtg ttt gtt	684
Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val	
195 200 205	
tta ggt gca gaa tac agg cat gaa aat ctt aaa gtg gtg cct ttt att	732
Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile	
210 215 220 225	
tta acg gac acc cgc ttg cct tta tcc acc caa aat gtt tta gtg caa	780
Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln	
230 235 240	
gtg ggg ggt aag ttg gag tat gac gct tct tta gct aag ggt ttc act	828
Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr	
245 250 255	
tcg cac act cta gtg cat ggc atg tat caa tac ggc aac act gat gcg	876
Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala	
260 265 270	
gct aca agc gtt aaa aat gcc ggc ttg ttt ttg atc gat caa act ttt	924
Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe	
275 280 285	
aaa tac aaa att ttt aat ttt gga acg ggt ttt tat atc gtt ccg gca	972
Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala	
290 295 300 305	
aga aac aat aag ggc tat cta tgg act ttt aat gac agg act aaa ttc	1020
Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe	
310 315 320	
tat ggc cgt ggg atc aat gcg ccc ggc gtg cca gcg att tat ttt gca	1068
Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala	
325 330 335	
aac tct agc att tca ggc tat gtt ttt tta ggg ctt aag act aaa agg	1116
Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg	
340 345 350	
gtg cgt tta gac gcg atg gtg gct ttt ggg gat tac caa gaa tat tct	1164
Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr Ser	
355 360 365	
tta atg agc agt ttt agg gtt tgg act tat agg agt ttg tct ttt gat	1212
Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe Asp	
370 375 380 385	

atg ggt ggg ggg tat gtg tat gct tac aat tct aaa gcc acg aga aaa 1260
Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg Lys
390 395 400

agt ctt gga aat agt tct ttt gtc ttt ttt ggg aag ttt ttg ttt 1305
Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe
405 410 415

taaaaaatac catttctaca atcaatagtg aagagtttgc aataaagtaa gc 1357

<210> 12

<211> 416

<212> PRT

<213> Helicobacter pylori

<400> 12

Met Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly
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Ile Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val
20 25 30
Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys
35 40 45
Asn Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe
50 55 60
Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp
65 70 75 80
Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly
85 90 95
Asn Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly
100 105 110
Asp Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile
115 120 125
Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly
130 135 140
Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg
145 150 155 160
Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile
165 170 175
Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala
180 185 190
Ser Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe
195 200 205
Val Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe
210 215 220
Ile Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val
225 230 235 240
Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe
245 250 255
Thr Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp
260 265 270
Ala Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr
275 280 285
Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro
290 295 300

Ala	Arg	Asn	Asn	Lys	Gly	Tyr	Leu	Trp	Thr	Phe	Asn	Asp	Arg	Thr	Lys
305					310					315					320
Phe	Tyr	Gly	Arg	Gly	Ile	Asn	Ala	Pro	Gly	Val	Pro	Ala	Ile	Tyr	Phe
				325					330					335	
Ala	Asn	Ser	Ser	Ile	Ser	Gly	Tyr	Val	Phe	Leu	Gly	Leu	Lys	Thr	Lys
				340				345					350		
Arg	Val	Arg	Leu	Asp	Ala	Met	Val	Ala	Phe	Gly	Asp	Tyr	Gln	Glu	Tyr
		355				360					365				
Ser	Leu	Met	Ser	Ser	Phe	Arg	Val	Trp	Thr	Tyr	Arg	Ser	Leu	Ser	Phe
	370					375					380				
Asp	Met	Gly	Gly	Gly	Tyr	Val	Tyr	Ala	Tyr	Asn	Ser	Lys	Ala	Thr	Arg
385					390					395					400
Lys	Ser	Leu	Gly	Asn	Ser	Ser	Phe	Val	Phe	Phe	Gly	Lys	Phe	Leu	Phe
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 aaaaggaaaa aa atg aaa aat agc acg cct tta aag aat caa gtt ttt tgt 111
 Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys
 1 5 10

ggg tta tat gtt tta agt ttg agc gct tct ttg caa gcg ttt gat tat 159
 Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr
 15 20 25

aaa att gaa gtt tca gcg gag tcc ttt tct aaa gtt ggc ttt aat aaa 207
 Lys Ile Glu Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys
 30 35 40 45

aaa aag att gat ata gct agg ggg att tat cct aca gag act ttt gta 255
 Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val
 50 55 60

acc gct gta ggg cag ggc aat atc tat gcg gat ttt tta ccc aaa ggc 303
 Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Pro Lys Gly
 65 70 75

ctt aaa gat caa ggg cat gtt tta gag gga aaa atc ggt ggc acg cta 351
 Leu Lys Asp Gln Gly His Val Leu Glu Gly Lys Ile Gly Gly Thr Leu
 80 85 90

gga ggg gtc gct tat gat agc acg aaa ttc aat caa ggc gga tcg gtt 399
 Gly Gly Val Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val
 95 100 105

att tat aac tac atc ggt tat tgg gat ggc tat tta ggg ggt aaa aga	447
Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg	
110 115 120 125	
gcc ttg ctt gat ggc acg agt atc cat gag tgc gcg ctt gga tct gat	495
Ala Leu Leu Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp	
130 135 140	
ggc aag gtg att gat tct ata gcg tgc ggg aac gct agg gcc aat aaa	543
Gly Lys Val Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys	
145 150 155	
atc cgc cgt aat tac ttg atg aat aac gct ttt tta gaa tac cgc tat	591
Ile Arg Arg Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr	
160 165 170	
aaa gat att ttt tta gct aag gga ggg cgt tat caa tcc aat gct cct	639
Lys Asp Ile Phe Leu Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro	
175 180 185	
tat atg agc ggt tac acg caa ggc ttt gaa atc agc gct aaa gtc aag	687
Tyr Met Ser Gly Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Val Lys	
190 195 200 205	
gat aaa aat gaa gga atc cac aaa tta tgg tgg ttt agc tca tgg ggt	735
Asp Lys Asn Glu Gly Ile His Lys Leu Trp Trp Phe Ser Ser Trp Gly	
210 215 220	
agg gcg ttc gct tat ggg gag tgg att tat gat ttt tat tct cca aga	783
Arg Ala Phe Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg	
225 230 235	
acc gtg gtt aaa aac ggg cgc act ttg aat tat ggt atc cat tta gtg	831
Thr Val Val Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val	
240 245 250	
aat tat act tat gaa aga aaa ggg gtt agc gtt agc cct ttt ttc caa	879
Asn Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln	
255 260 265	
ttt tcg cct ggg act tat tat agc cct ggg gtg gtt gta ggc tat gat	927
Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp	
270 275 280 285	
agt aac cct aat ttt aac ggc gtt ggc ttt aga tcc gaa aca aaa gct	975
Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala	
290 295 300	
tat att ttg ctc cct gtc cat gac ccc tta aga agg gat act tat cgt	1023
Tyr Ile Leu Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg	
305 310 315	
tac gct ata aag gct ggc act gcc ggg caa agc ttg ctc att agg caa	1071
Tyr Ala Ile Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln	
320 325 330	

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65				70						75					80
Gln	Gly	His	Val	Leu	Glu	Gly	Lys	Ile	Gly	Gly	Thr	Leu	Gly	Gly	Val
			85						90					95	
Ala	Tyr	Asp	Ser	Thr	Lys	Phe	Asn	Gln	Gly	Gly	Ser	Val	Ile	Tyr	Asn
			100					105					110		
Tyr	Ile	Gly	Tyr	Trp	Asp	Gly	Tyr	Leu	Gly	Gly	Lys	Arg	Ala	Leu	Leu
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Asp	Gly	Thr	Ser	Ile	His	Glu	Cys	Ala	Leu	Gly	Ser	Asp	Gly	Lys	Val
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145					150					155					160
Asn	Tyr	Leu	Met	Asn	Asn	Ala	Phe	Leu	Glu	Tyr	Arg	Tyr	Lys	Asp	Ile
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Phe	Leu	Ala	Lys	Gly	Gly	Arg	Tyr	Gln	Ser	Asn	Ala	Pro	Tyr	Met	Ser
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Gly	Tyr	Thr	Gln	Gly	Phe	Glu	Ile	Ser	Ala	Lys	Val	Lys	Asp	Lys	Asn
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Glu	Gly	Ile	His	Lys	Leu	Trp	Trp	Phe	Ser	Ser	Trp	Gly	Arg	Ala	Phe
210						215					220				
Ala	Tyr	Gly	Glu	Trp	Ile	Tyr	Asp	Phe	Tyr	Ser	Pro	Arg	Thr	Val	Val
225					230					235					240
Lys	Asn	Gly	Arg	Thr	Leu	Asn	Tyr	Gly	Ile	His	Leu	Val	Asn	Tyr	Thr
				245					250					255	
Tyr	Glu	Arg	Lys	Gly	Val	Ser	Val	Ser	Pro	Phe	Phe	Gln	Phe	Ser	Pro
			260					265					270		
Gly	Thr	Tyr	Tyr	Ser	Pro	Gly	Val	Val	Val	Gly	Tyr	Asp	Ser	Asn	Pro
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Asn	Phe	Asn	Gly	Val	Gly	Phe	Arg	Ser	Glu	Thr	Lys	Ala	Tyr	Ile	Leu
290						295					300				
Leu	Pro	Val	His	Asp	Pro	Leu	Arg	Arg	Asp	Thr	Tyr	Arg	Tyr	Ala	Ile
305					310					315					320
Lys	Ala	Gly	Thr	Ala	Gly	Gln	Ser	Leu	Leu	Ile	Arg	Gln	Arg	Phe	Asp
				325					330					335	
Tyr	Asn	Glu	Phe	Asn	Phe	Gly	Gly	Ala	Phe	Tyr	Lys	Val	Trp	Lys	Asn
			340					345					350		
Ala	Asn	Ala	Tyr	Ile	Gly	Thr	Thr	Gly	Asn	Pro	Leu	Gly	Ile	Asp	Phe
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Trp	Thr	Asn	Ser	Val	Tyr	Asp	Ile	Gly	Gln	Ala	Leu	Ser	His	Val	Val
370						375					380				
Thr	Ala	Asp	Ala	Val	Ser	Gly	Trp	Val	Phe	Gly	Gly	Gly	Val	His	Lys
385					390					395					400
Lys	Trp	Leu	Trp	Gly	Thr	Leu	Trp	Arg	Trp	Thr	Ser	Gly	Thr	Leu	Ala
			405						410					415	
Asn	Glu	Ala	Ser	Ala	Ala	Val	Asn	Val	Gly	Tyr	Lys	Ile	Ser	Lys	Ser
			420					425					430		
Leu	Thr	Ala	Ser	Val	Lys	Leu	Glu	Tyr	Leu	Gly	Val	Met	Thr	His	Ala
		435					440					445			
Gly	Phe	Thr	Val	Gly	Ser	Tyr	Arg	Pro	Thr	Pro	Gly	Ser	Lys	Ala	Leu
	450					455					460				
Tyr	Ser	Asp	Arg	Ser	His	Leu	Met	Thr	Thr	Leu	Ser	Ala	Lys	Phe	
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 Met Asn Lys Thr Thr Val
 1 5

aaa ata tta atg ggc atg gcg tta tta tca tcg ctt caa gcc gca gag 163
 Lys Ile Leu Met Gly Met Ala Leu Leu Ser Ser Leu Gln Ala Ala Glu
 10 15 20

gca gag ctt gat gaa aaa tca aaa aaa cct aaa ttt gcg gac agg aat 211
 Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro Lys Phe Ala Asp Arg Asn
 25 30 35

aca ttt tat tta ggg gtt ggg tat caa ctt agt gcg atc aac aca tct 259
 Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu Ser Ala Ile Asn Thr Ser
 40 45 50

ttt agc acc gag tct gta gat aaa tcg tat ttt atg acc ggc aat ggc 307
 Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr Phe Met Thr Gly Asn Gly
 55 60 65 70

ttt ggt gtg gtg tta ggg ggg aaa ttt gtg gct aaa acg caa gct gta 355
 Phe Gly Val Val Leu Gly Gly Lys Phe Val Ala Lys Thr Gln Ala Val
 75 80 85

gag cat gtg ggt ttc cgt tac ggg ttg ttt tat gat cag acc ttt tct 403
 Glu His Val Gly Phe Arg Tyr Gly Leu Phe Tyr Asp Gln Thr Phe Ser
 90 95 100

tct cac aaa tcc tat att tct acc tat ggt tta gaa ttt agc ggt ttg 451
 Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly Leu Glu Phe Ser Gly Leu
 105 110 115

tgg gac gct ttc aat tcg cca aag atg ttt tta ggg tta gag ttt ggc 499
 Trp Asp Ala Phe Asn Ser Pro Lys Met Phe Leu Gly Leu Glu Phe Gly
 120 125 130

tta ggc atc gct ggg gcg act tat atg cca gga ggg gct atg cat ggg 547
 Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro Gly Gly Ala Met His Gly
 135 140 145 150

att atc gct caa aat tta ggc aaa gaa aat tcg ctt ttc caa ttg ctt 595
 Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn Ser Leu Phe Gln Leu Leu
 155 160 165

gtg aaa gtg ggt ttt cgt ttt ggc ttt ttg cac aat gaa atc act ttc 643
Val Lys Val Gly Phe Arg Phe Gly Phe Leu His Asn Glu Ile Thr Phe
170 175 180

ggg ttg aaa ttc cct gtc att cct aac aaa aga acg gaa atc att gat 691
Gly Leu Lys Phe Pro Val Ile Pro Asn Lys Arg Thr Glu Ile Ile Asp
185 190 195

ggc ttg agc acg act act tta tgg cac cgc tta ccg gta gct tat ttc 739
Gly Leu Ser Thr Thr Thr Leu Trp His Arg Leu Pro Val Ala Tyr Phe
200 205 210

aat tat atc tat aat ttt tagatatggt tatttagagg ttttagattt 787
Asn Tyr Ile Tyr Asn Phe
215 220

gacaaaatca atcaactctc gtg 810

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<213> Helicobacter pylori

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Lys Phe Ala Asp Arg Asn Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu
35 40 45
Ser Ala Ile Asn Thr Ser Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr
50 55 60
Phe Met Thr Gly Asn Gly Phe Gly Val Val Leu Gly Gly Lys Phe Val
65 70 75 80
Ala Lys Thr Gln Ala Val Glu His Val Gly Phe Arg Tyr Gly Leu Phe
85 90 95
Tyr Asp Gln Thr Phe Ser Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly
100 105 110
Leu Glu Phe Ser Gly Leu Trp Asp Ala Phe Asn Ser Pro Lys Met Phe
115 120 125
Leu Gly Leu Glu Phe Gly Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro
130 135 140
Gly Gly Ala Met His Gly Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn
145 150 155 160
Ser Leu Phe Gln Leu Leu Val Lys Val Gly Phe Arg Phe Gly Phe Leu
165 170 175
His Asn Glu Ile Thr Phe Gly Leu Lys Phe Pro Val Ile Pro Asn Lys
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Arg Thr Glu Ile Ile Asp Gly Leu Ser Thr Thr Thr Leu Trp His Arg
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180	185	190	
gcg ttc gct tac ggc tcg ttt ttg atg gat tgg ttt gcc gct agg acc			680
Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr			
195	200	205	210
act tat agc gga ggt ttt acc aaa aac gat aag gga ggt tat gat agc			728
Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser			
	215	220	225
cat ggg cga aag gtg ctt tat ggc acg cat gcg gtg caa ctc acc tat			776
His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr			
	230	235	240
aaa cct cat cgt ttc ctc ata gaa ggc ttt tat tac ctt tcg cct caa			824
Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln			
	245	250	255
atc ttt aac gct ccg ggc gtt aag att ggt tgg gat tct aac cct aat			872
Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn			
	260	265	270
ttt agc ggc aca ggc ttt cgc tct gat aca gct atc ata ggg ttt ttc			920
Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe			
275	280	285	290
ccc att tac tac cct tgg atg atc gtt aaa tcc aat gga agc ccg gtc			968
Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val			
	295	300	305
tat aaa tac gac acg cct gcc act caa aat ggg caa aac ctc att atc			1016
Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile			
	310	315	320
ctc caa cgc ttt gac atc aac aat tac aat gtt tcc atc gct ttt tat			1064
Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr			
	325	330	335
aaa gtc ttt caa aac gct aat ggt tgg ata ggc aac atg ggg aat cca			1112
Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro			
	340	345	350
agc ggt gtg atc atg ggg agt aac agc gtc tat gcg ggt ttt aca ggc			1160
Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly			
355	360	365	370
aca gcc ctt aaa aga gat gcc gct acc att ttc ctt tct tgt ggc ggc			1208
Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly			
	375	380	385
act cat ttt gcc aaa aaa ttc aca tgg aaa ttc gcc acg caa tac tcc			1256

Thr	His	Phe	Ala	Lys	Lys	Phe	Thr	Trp	Lys	Phe	Ala	Thr	Gln	Tyr	Ser		
			390					395					400				
aat	tca	gtg	ggt	tct	tgg	gaa	gcg	aga	gcg	atg	atc	tct	tta	ggg	tat	1304	
Asn	Ser	Val	Val	Ser	Trp	Glu	Ala	Arg	Ala	Met	Ile	Ser	Leu	Gly	Tyr		
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aaa	ttc	act	gaa	tac	ttg	agc	ggg	agc	gtg	gat	ctt	gca	tat	tat	ggc	1352	
Lys	Phe	Thr	Glu	Tyr	Leu	Ser	Gly	Ser	Val	Asp	Leu	Ala	Tyr	Tyr	Gly		
		420				425					430						
gtg	tat	act	aac	aaa	gga	ttt	aaa	ccg	ggg	gaa	aac	ggg	cct	gtg	cct	1400	
Val	Tyr	Thr	Asn	Lys	Gly	Phe	Lys	Pro	Gly	Glu	Asn	Gly	Pro	Val	Pro		
435					440					445					450		
aaa	gac	ttc	ccc	gcc	ctt	tat	tct	gac	agg	agc	gcg	tta	tac	acg	gct	1448	
Lys	Asp	Phe	Pro	Ala	Leu	Tyr	Ser	Asp	Arg	Ser	Ala	Leu	Tyr	Thr	Ala		
				455				460						465			
cta	gta	gca	tct	ttt	tgatgctacc	ctatgattat	gggtgggcgctc	ttttgatgct	1503								
Leu	Val	Ala	Ser	Phe													
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Ser	Thr	Ile	Gly	Phe	Asn	Gln	His	Lys	Ile	Asn	Lys	Glu	Arg	Gly	Ile		
		35				40						45					
Tyr	Pro	Met	Gln	Gln	Phe	Ala	Thr	Ile	Ala	Gly	Tyr	Leu	Gly	Leu	Gly		
	50					55					60						
Phe	Ser	Leu	Leu	Pro	Lys	Lys	Val	Ser	Asp	His	Val	Leu	Lys	Gly	Lys		
65					70				75						80		
Ile	Gly	Gly	Met	Val	Gly	Ser	Ile	Phe	Tyr	Asp	Gly	Thr	Lys	Lys	Phe		
			85					90					95				
Glu	Asp	Ser	Ser	Val	Ala	Tyr	Asn	Leu	Phe	Gly	Tyr	Tyr	Asp	Gly	Phe		
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145					150					155					160		
Tyr	Leu	Ser	Thr	Met	Pro	Tyr	Lys	Ser	Gly	Gln	Thr	Gln	Gly	Phe	Gln		
			165						170					175			
Ile	Ser	Gly	Gln	Tyr	Lys	Lys	Ala	Arg	Leu	Thr	Trp	Phe	Ser	Ser	Phe		
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Arg	Thr	Thr	Tyr	Ser	Gly	Gly	Phe	Thr	Lys	Asn	Asp	Lys	Gly	Gly	Tyr		
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225					230					235					240		
Thr	Tyr	Lys	Pro	His	Arg	Phe	Leu	Ile	Glu	Gly	Phe	Tyr	Tyr	Leu	Ser		
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Pro	Gln	Ile	Phe	Asn	Ala	Pro	Gly	Val	Lys	Ile	Gly	Trp	Asp	Ser	Asn		
			260				265						270				
Pro	Asn	Phe	Ser	Gly	Thr	Gly	Phe	Arg	Ser	Asp	Thr	Ala	Ile	Ile	Gly		
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Phe	Phe	Pro	Ile	Tyr	Tyr	Pro	Trp	Met	Ile	Val	Lys	Ser	Asn	Gly	Ser		
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Pro	Val	Tyr	Lys	Tyr	Asp	Thr	Pro	Ala	Thr	Gln	Asn	Gly	Gln	Asn	Leu		
305					310					315					320		
Ile	Ile	Leu	Gln	Arg	Phe	Asp	Ile	Asn	Asn	Tyr	Asn	Val	Ser	Ile	Ala		
				325					330					335			
Phe	Tyr	Lys	Val	Phe	Gln	Asn	Ala	Asn	Gly	Trp	Ile	Gly	Asn	Met	Gly		
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		355				360						365					
Thr	Gly	Thr	Ala	Leu	Lys	Arg	Asp	Ala	Ala	Thr	Ile	Phe	Leu	Ser	Cys		
	370					375					380						
Gly	Gly	Thr	His	Phe	Ala	Lys	Lys	Phe	Thr	Trp	Lys	Phe	Ala	Thr	Gln		
385					390					395					400		
Tyr	Ser	Asn	Ser	Val	Val	Ser	Trp	Glu	Ala	Arg	Ala	Met	Ile	Ser	Leu		
			405					410					415				
Gly	Tyr	Lys	Phe	Thr	Glu	Tyr	Leu	Ser	Gly	Ser	Val	Asp	Leu	Ala	Tyr		
		420					425					430					
Tyr	Gly	Val	Tyr	Thr	Asn	Lys	Gly	Phe	Lys	Pro	Gly	Glu	Asn	Gly	Pro		
	435					440						445					
Val	Pro	Lys	Asp	Phe	Pro	Ala	Leu	Tyr	Ser	Asp	Arg	Ser	Ala	Leu	Tyr		
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 Met Lys Lys Thr Lys Lys Thr Ile Leu

1

5

ctt tct cta act ctc gcg gcg tca ttg ctc cat gct gaa gac aac ggc 161
 Leu Ser Leu Thr Leu Ala Ala Ser Leu Leu His Ala Glu Asp Asn Gly
 10 15 20 25

gtt ttt tta agc gtg ggt tat caa atc ggt gaa gcg gtt caa aaa gtg 209
 Val Phe Leu Ser Val Gly Tyr Gln Ile Gly Glu Ala Val Gln Lys Val
 30 35 40

aaa aac gcc gac aag gtg caa aaa ctt tca gac act tat gaa caa tta 257
 Lys Asn Ala Asp Lys Val Gln Lys Leu Ser Asp Thr Tyr Glu Gln Leu
 45 50 55

agc cgg ctt tta acc aac gat aat ggc aca aac tca aag aca agc gcg 305
 Ser Arg Leu Leu Thr Asn Asp Asn Gly Thr Asn Ser Lys Thr Ser Ala
 60 65 70

caa nat caa cca agc ggt taataatttg aacgaacgcg caaaaacttt 353
 Gln Xaa Gln Pro Ser Gly
 75

agccggtggg acaaccaatt cccc 377

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<212> PRT

<213> Helicobacter pylori

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<222> 75

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 Gln Ile Gly Glu Ala Val Gln Lys Val Lys Asn Ala Asp Lys Val Gln
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<213> Helicobacter pylori

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Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
1 5 10 15
gac gct aaa gaa atc gct atg caa cga ttt gac aaa caa aac cat aag 155
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
20 25 30
att ttt gaa atc ctt gcg gat aaa gtg agc gct aaa gac aat gtg ata 203
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
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acc gca tca ggg aat gcg atc tta ttg aat tat gat gtg tat att cta 251
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
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gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta tta gag 299
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
65 70 75 80
ggg aat atc aag gtt tat agg ggc gag ggt ttg ctc gtt aaa acc gat 347
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
85 90 95
tac gtg aaa ttg agt ttg aat gaa aaa tat gaa atc att ttc ccc ttt 395
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
100 105 110
tat gtc caa gac agc gtg agc ggg att tgg gtg agc gcg gat att gcc 443
Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
115 120 125
agc gga aag gat caa aaa tat aag gtt aaa aac atg agc act tca ggg 491
Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
130 135 140
tgc agc att gat aac ccc att tgg cat gtc aat gcg act tca ggc tca 539
Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
145 150 155 160
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Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr
165 170 175
gtc ggt gat att cct gta ttg tat ttg ccc tat att ttc atg tcc acg 635
Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr
180 185 190
agc aat aaa aga act act ggg ttt tta tac cct gag ttt ggc act tcc 683
Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser
195 200 205
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Phe	Gly	Leu	Asn	Phe	Glu	Ala	Arg	Tyr	Ile	Asn	Ser	Lys	Asn	Asp	Arg		
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Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser		
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tct	agc	agg	gac	act	tta	caa	aaa	tac	ttc	cac	ctt	aag	tct	aat	att	971	
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile		
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Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr		
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gtg	cgt	ttt	gaa	aag	gtt	aat	aag	cgt	atc	aca	gac	gcc	acg	cac	atg	1067	
Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met		
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Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu		
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Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr		
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Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu		
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Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr		
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Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro		
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Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu		
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Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn	
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tcc ttc gtg cct acg atc cct aat gaa tca agg gaa ttt ggg aat ttt	1451
Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe	
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Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu	
465 470 475 480	
tac aac aag ctt ttc cac acg atc caa cta gaa gcg att ttc aac atc	1547
Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile	
485 490 495	
cct tat tac acc ttt aaa aac ggc tta ttt tct caa aac atg tat gct	1595
Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala	
500 505 510	
tta agc gcg caa gcc tta aac agc tac act tcg cct tta ttg aga gat	1643
Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp	
515 520 525	
tat gat tat caa ggg cgt ttg tat gac tcg gtg tgg aat cct agc agt	1691
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser	
530 535 540	
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Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr	
545 550 555 560	
caa tac ctt tat ggc tta ggg ggg caa gag tta ttg tat ttt aaa ata	1787
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile	
565 570 575	
tcg caa ctc atc aat ctt gac gat aaa gtt tcg ccc ttt aga atg cca	1835
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro	
580 585 590	
cta gag agc aag atc ggg ttt tcg ccc tta acg gga ttg aac atc ttt	1883
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe	
595 600 605	
ggg aat gtc ttt tat tcg ttt tat caa aac cgc tta gaa gaa atc tct	1931
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser	
610 615 620	
gtg aac gcc aat tac caa cgc aag ttt tta agc ttt aac ctc tct tat	1979
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr	
625 630 635 640	
ttt tta aaa aac aat ttt agc agt ggg att aat agc att gta gaa aat	2027
Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn	
645 650 655	

ctg cgg att att taaaggcggg ttttagcaac gactttggct atttttccat 2079
 Leu Arg Ile Ile
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 <213> *Helicobacter pylori*

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 35 40 45
 Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
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 Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
 65 70 75 80
 Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
 85 90 95
 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
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 Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
 115 120 125
 Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
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 Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
 145 150 155 160
 Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr
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 Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr
 180 185 190
 Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser
 195 200 205
 Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys
 210 215 220
 Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly
 225 230 235 240
 Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg
 245 250 255
 Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys
 260 265 270
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser
 275 280 285
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile
 290 295 300
 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr
 305 310 315 320
 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met

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Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr		
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Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu		
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Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr		
385					390				395						400		
Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro		
			405						410					415			
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Tyr	Leu	Ser	Leu	Gly	Leu			
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Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	Lys	Asn		
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Pro	Tyr	Tyr	Thr	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	Tyr	Ala		
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Leu	Ser	Ala	Gln	Ala	Leu	Asn	Ser	Tyr	Thr	Ser	Pro	Leu	Leu	Arg	Asp		
	515					520					525						
Tyr	Asp	Tyr	Gln	Gly	Arg	Leu	Tyr	Asp	Ser	Val	Trp	Asn	Pro	Ser	Ser		
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Leu	Glu	Ser	Lys	Ile	Gly	Phe	Ser	Pro	Leu	Thr	Gly	Leu	Asn	Ile	Phe		
	595					600					605						
Gly	Asn	Val	Phe	Tyr	Ser	Phe	Tyr	Gln	Asn	Arg	Leu	Glu	Glu	Ile	Ser		
	610					615				620							
Val	Asn	Ala	Asn	Tyr	Gln	Arg	Lys	Phe	Leu	Ser	Phe	Asn	Leu	Ser	Tyr		
625				630				635						640			
Phe	Leu	Lys	Asn	Asn	Phe	Ser	Ser	Gly	Ile	Asn	Ser	Ile	Val	Glu	Asn		
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Leu	Arg	Ile	Ile														
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Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val Val Leu
5 10 15

tgc ggt gca atg gct aat acg gct ata gct ggt cct aaa ata gaa gca 152
Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile Glu Ala
20 25 30

agg ggt gag ttt ggc aga ttt tgg ggg gga gct gtt ggt ggt gca att 200
Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly Ala Ile
35 40 45 50

ggg ggt ggt gtt ggt ggt gca gtg ggg gga gct gtt ggt ggt cct gcg 248
Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala
55 60 65

ggt ggt tgg gct ggc aga tta gtt ggt ggt tct gtg ggg aga gag ttt 296
Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe
70 75 80

ggt cgg gaa ata ggc gat agg gta gaa gat tac atc cgt ggc gtt gat 344
Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp
85 90 95

aga gag cca caa gcc cca aga gaa ccc acc tat gat cgt cat ttc gtg 392
Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val
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Tyr Asp Arg
115

tcgtttgagc gat 454

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35 40 45
Ala Ile Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly
50 55 60
Pro Ala Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg
65 70 75 80
Glu Phe Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly

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Val	Asp	Arg	Glu	Pro	Gln	Ala	Pro	Arg	Glu	Pro	Thr	Tyr	Asp	Arg	His				
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Phe	Val	Tyr	Asp	Arg															
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Met	Leu	Lys	Arg	Met	Ile	Leu	Leu	Gly	Ala	Leu	Gly	Val	Leu	Ala	Ser			
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gct	gaa	gag	agt	gcg	gct	ttt	gtg	gga	gtc	aat	tac	cag	gtg	agc	atg			154
Ala	Glu	Glu	Ser	Ala	Ala	Phe	Val	Gly	Val	Asn	Tyr	Gln	Val	Ser	Met			
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ata	caa	aat	cag	act	aaa	atg	gtg	aat	gac	aac	ggc	ttg	caa	aag	cct			202
Ile	Gln	Asn	Gln	Thr	Lys	Met	Val	Asn	Asp	Asn	Gly	Leu	Gln	Lys	Pro			
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Leu	Ile	Lys	Phe	Pro	Pro	Tyr	Ala	Gly	Ala	Gly	Phe	Glu	Val	Gly	Tyr			
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aag	caa	ttt	ttt	ggg	aag	aaa	aaa	tgg	ttt	ggc	atg	cgt	tat	tat	ggg			298
Lys	Gln	Phe	Phe	Gly	Lys	Lys	Lys	Trp	Phe	Gly	Met	Arg	Tyr	Tyr	Gly			
	65				70				75						80			
ttt	ttt	gac	tac	gcg	cac	aac	cgc	ttt	ggc	gtg	atg	aaa	aag	ggc	att			346
Phe	Phe	Asp	Tyr	Ala	His	Asn	Arg	Phe	Gly	Val	Met	Lys	Lys	Gly	Ile			
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ccg	gtg	ggc	gat	agt	ggg	ttt	att	tac	aat	agt	ttt	agt	ttt	gga	ggg			394
Pro	Val	Gly	Asp	Ser	Gly	Phe	Ile	Tyr	Asn	Ser	Phe	Ser	Phe	Gly	Gly			
			100					105					110					
aac	act	tta	acg	gaa	agg	gat	tcc	tat	cag	ggg	caa	tac	tat	gtc	aat			442
Asn	Thr	Leu	Thr	Glu	Arg	Asp	Ser	Tyr	Gln	Gly	Gln	Tyr	Tyr	Val	Asn			
		115					120					125						
tta	ttc	act	tat	ggc	gtg	ggg	tta	gat	acg	ctg	tgg	aat	ttt	gtg	aat			490
Leu	Phe	Thr	Tyr	Gly	Val	Gly	Leu	Asp	Thr	Leu	Trp	Asn	Phe	Val	Asn			
	130					135					140							
aaa	gaa	aac	atg	gtt	ttt	ggg	ttt	gtg	gtg	ggg	atc	caa	tta	gcg	ggg			538

Lys	Glu	Asn	Met	Val	Phe	Gly	Phe	Val	Val	Gly	Ile	Gln	Leu	Ala	Gly		
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gat	agt	tgg	gca	acg	agc	atc	agt	aaa	gaa	atc	gct	cat	tat	gca	aaa	586	
Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	Glu	Ile	Ala	His	Tyr	Ala	Lys		
				165					170					175			
cac	cac	agc	aat	tcc	agt	tat	agc	ccg	gcc	aat	ttc	cag	ttt	tta	tgg	634	
His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	Ala	Asn	Phe	Gln	Phe	Leu	Trp		
			180					185					190				
aag	ttt	ggg	gtc	cgc	acc	cat	atc	gct	aaa	cac	aat	agc	cta	gaa	tta	682	
Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala	Lys	His	Asn	Ser	Leu	Glu	Leu		
		195					200					205					
ggg	att	aaa	gtg	cct	acg	atc	aca	cac	cag	ctt	ttc	tct	ctt	acc	aac	730	
Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	Gln	Leu	Phe	Ser	Leu	Thr	Asn		
		210				215					220						
gaa	aag	gga	tac	acc	tta	cag	gct	gat	gtg	cgt	aga	ggt	tat	gcg	ttt	778	
Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp	Val	Arg	Arg	Val	Tyr	Ala	Phe		
225					230					235					240		
caa	atc	agt	tac	ttg	agg	gat	ttt	taaccccttt	ttagatacaa	tcacgcctga	832						
Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe										
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Ile	Gln	Asn	Gln	Thr	Lys	Met	Val	Asn	Asp	Asn	Gly	Leu	Gln	Lys	Pro		
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Leu	Ile	Lys	Phe	Pro	Pro	Tyr	Ala	Gly	Ala	Gly	Phe	Glu	Val	Gly	Tyr		
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Lys	Gln	Phe	Phe	Gly	Lys	Lys	Lys	Trp	Phe	Gly	Met	Arg	Tyr	Tyr	Gly		
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Pro	Val	Gly	Asp	Ser	Gly	Phe	Ile	Tyr	Asn	Ser	Phe	Ser	Phe	Gly	Gly		
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Leu	Phe	Thr	Tyr	Gly	Val	Gly	Leu	Asp	Thr	Leu	Trp	Asn	Phe	Val	Asn		
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Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	Glu	Ile	Ala	His	Tyr	Ala	Lys
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His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	Ala	Asn	Phe	Gln	Phe	Leu	Trp
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Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	Gln	Leu	Phe	Ser	Leu	Thr	Asn
	210					215				220					
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<213> Helicobacter pylori

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Val	Ala	Ser	Asn	Leu	Gln	Ala	Gln	Glu	Thr	Thr	His	Thr	Leu	Gly	Lys	
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Val	Thr	Thr	Lys	Gly	Glu	Arg	Thr	Phe	Glu	Tyr	Asn	Asn	Lys	Met	Tyr	
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Ile	Phe	Arg	Thr	Arg	Ala	Asp	Val	Asn	Val	Ala	Ser	Gly	Gly	Leu	Met	
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gcg	caa	aag	atc	tat	gtt	agg	ggg	att	gag	agc	cgt	ctc	tta	agg	gta	350
Ala	Gln	Lys	Ile	Tyr	Val	Arg	Gly	Ile	Glu	Ser	Arg	Leu	Leu	Arg	Val	
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aca	ata	gat	ggc	gtc	gcc	caa	aat	ggt	aac	att	ttc	cac	cat	gac	gct	398
Thr	Ile	Asp	Gly	Val	Ala	Gln	Asn	Gly	Asn	Ile	Phe	His	His	Asp	Ala	
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Ile	Asp	Pro	Asn	Asp	Pro	Asn	Gly	Pro	Gly	Leu	Pro	Tyr	Arg	His	Tyr	
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Tyr	Thr	Asp	Gln	Ser	Ser	Gln	Tyr	Pro	Gln	Asn	Leu	Asn	Thr	Pro	Asn	
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Thr Lys Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr	
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Val Ile Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu	
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Phe Tyr Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr	
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Arg Tyr Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro	
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 785 790 795

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 Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln
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 Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala Asn Thr
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 Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu Ser Phe
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 Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr Tyr Gly
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 Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg Met Asn
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Lys Asn Phe Leu Gly Thr Phe	Ser Val Ala Arg Ser Trp	Pro Thr Ala
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Arg Gly His Leu Leu Ala Asp	Thr Tyr Ala Leu Ala	Ala Thr Thr Gly
740	745	750
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755	760	765
Thr Leu Thr Trp Leu Ser Arg	Phe Val Thr Asn Met	Tyr Tyr Glu Gly
770	775	780
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Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu	
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aaa gcc gat gat ttt tta gaa gaa gcg aac gaa aca gcc ccg gcg cat	152
Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro Ala His	

20	25	30	
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Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe			
35	40	45	50
gac aaa aac cgc tca aaa atg tcc aac act ttg aac att gat tac ttt			248
Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe			
	55	60	65
caa ggg caa act tat aaa atc ccg ctt gcg tta tgc gat ggc gmc ctt			296
Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu			
	70	75	80
att gtt ttt ttc aaa acc cat tagcgatttt gttttagggg ataagggtggg			347
Ile Val Phe Phe Lys Thr His			
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 35 40 45
 Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
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Lys	Val	Phe	Leu	Gly	Met	Ala	Leu	Ala	Phe	Ser	Val	Ser	Met	Ala	Glu		
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Lys	Ser	Gly	Ala	Phe	Leu	Gly	Gly	Gly	Phe	Gln	Tyr	Ser	Asn	Leu	Glu		
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Asn	Gln	Asn	Thr	Thr	Arg	Thr	Pro	Gly	Ala	Asn	Asn	Asn	Thr	Pro	Ile		
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gac	act	tca	atg	ttt	ggc	agc	aac	aaa	aca	gct	cca	gcc	caa	gaa	acg		248
Asp	Thr	Ser	Met	Phe	Gly	Ser	Asn	Lys	Thr	Ala	Pro	Ala	Gln	Glu	Thr		
				55					60					65			
caa	agc	gct	tcc	aaa	ccg	gac	act	aaa	gtc	aat	cca	agc	gca	agt	tgg		296
Gln	Ser	Ala	Ser	Lys	Pro	Asp	Thr	Lys	Val	Asn	Pro	Ser	Ala	Ser	Trp		
			70					75					80				
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Leu	Glu	Asn	Gln	Asn	Thr	Thr	Arg	Thr	Pro	Gly	Ala	Asn	Asn	Asn	Thr		
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Pro	Ile	Asp	Thr	Ser	Met	Phe	Gly	Ser	Asn	Lys	Thr	Ala	Pro	Ala	Gln		
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Glu	Thr	Gln	Ser	Ala	Ser	Lys	Pro	Asp	Thr	Lys	Val	Asn	Pro	Ser	Ala		
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Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu
      5                      10                      15

tca gca gag acc cct aag caa gaa aaa gct att aag act agc cct acc      152
Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr
      20                      25                      30

aaa aaa ggt gaa aga aat gct gct ttt ata ggg att gat tac cag ttg      200
Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu
      35                      40                      45                      50

ggt atg ctc agc act acc gct caa aat tgt tcc cat ggg aat tgc aat      248
Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn
      55                      60                      65

ggt aat caa agt ggg gct tac ggc tct aat acg cct aac atg cct aca      296
Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr
      70                      75                      80

gcg tca aac cca aca gga ggg ttt act cat ggc gct cta ggg act cgt      344
Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg
      85                      90                      95

ggg tat aaa ggc tta agc aac caa caa tac gct atc aat ggt ttt ggt      392
Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly
      100                      105                      110

ttt gtt gta ggg tat aag cat ttt ttc aag aaa tcc ccg caa ttt gga      440
Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly
      115                      120                      125                      130

atg cgt tat tac gga ttc ttt gat ttt gca agc tct tat tat aag tat      488
Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr Lys Tyr
      135                      140                      145

tac act tat aat gat tat ggc atg aga gac gct cgc aag ggt tct caa      536
Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly Ser Gln
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agt ttc atg ttt ggc tat ggg gct ggc aca gat gtg ttg ttt aac ccg      584
Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe Asn Pro
      165                      170                      175

gct att ttc aat cgt gag aac ttg cat ttt ggg ttt ttc ttg ggc gtt      632
Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu Gly Val
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180	185	190	
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195	200	205	210
ttg gct gat gag tat aga ggg agt ttc cac cca tca aat ttc cag gtc			728
Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe Gln Val			
	215	220	225
tta gtt aat ggt ggg att cgc tta ggc act aaa cac caa ggt ttt gaa			776
Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly Phe Glu			
	230	235	240
att ggc ttg aaa atc caa acc atc cgc aac aat tac tac acc gct agt			824
Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr Ala Ser			
	245	250	255
gcg gat aat gtg cct gaa ggg act act tat aga ttc act ttc cac cgc			872
Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe His Arg			
	260	265	270
ccc tat gcc ttt tat tgg cgt tac att gta agc ttt taagggtgttt			918
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35 40 45			
Gln Leu Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn			
50 55 60			
Cys Asn Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met			
65 70 75 80			
Pro Thr Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly			
85 90 95			
Thr Arg Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly			
100 105 110			
Phe Gly Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln			
115 120 125			
Phe Gly Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr			
130 135 140			
Lys Tyr Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly			
145 150 155 160			
Ser Gln Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe			

gcg ggt atc ttt tgg caa tat att ggt tgg tat gcg ggg cat agt ggt	489
Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His Ser Gly	
135 140 145	
ttg caa gtg caa aaa cct cgt tta gcc atg gtg cat aac gct ttt ttg	537
Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala Phe Leu	
150 155 160	
agc tac aac tac aaa aaa gac aaa ttc agt ttt ggc gtg aaa ggg ggg	585
Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys Gly Gly	
165 170 175	
cgc tat gac gct gaa gag tat gat tgg ttc act tct tac act caa ggg	633
Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr Gln Gly	
180 185 190	
gtt gaa ggc ttt gtc aaa tat aaa gac acc aga ttc agg gtg atg tat	681
Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val Met Tyr	
195 200 205 210	
tca gac gct agg gct tca gcg tca agc gac tgg ttt tgg tat ttt ggg	729
Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr Phe Gly	
215 220 225	
cgt tac tat aca agc ggt aag gct cta atg gta gct gat ttg aaa tat	777
Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu Lys Tyr	
230 235 240	
gaa aaa gac aac cta aaa atc aac cct tat ttt tat gcg atc ttt caa	825
Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile Phe Gln	
245 250 255	
aga atg tat gcg cca ggc att aat atc act tat gac acc aac cct aat	873
Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn Pro Asn	
260 265 270	
ttc aac aat aag ggt ttt cgt ttt gta ggc act ttc gta ggg ttt ttc	921
Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly Phe Phe	
275 280 285 290	
ccc att ttt gcc act ccg gct aat caa aat gat att atc ctc ttc caa	969
Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu Phe Gln	
295 300 305	
caa gtg cca tta ggc aag agt ggg caa act tat ttc ttc cgc act cgt	1017
Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg Thr Arg	
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Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys Asn Ile	
325 330 335	
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Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu Gly Tyr	

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Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn Ile Val			
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Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln Tyr Arg			
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Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro Arg Ala			
	390	395	400
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Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn Lys Tyr			
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aat att aga atg gat tta aaa cta gaa tat tat ggc aat atc acc aaa			1353
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aaa ggc tat tgt att ggg tat tgt ggc atg tat gtt cca gtc gat cct			1401
Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val Asp Pro			
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agc cat ata atg ttt aac att gct tac ggt ttt agg att tac			1491
Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr			
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Ser Leu Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile			
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50 55 60			
Tyr Gln Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu			
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-46-

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Leu	Gly	Phe	Ser	Ala	Cys	Lys	Asn	Ser	Gln	Lys	Ser	Gln	Asp	Ser	Gln	
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Asn	Asn	Thr	Pro	Gln	Gln	Asp	Ser	Pro	Lys	Thr	Tyr	Thr	Ala	Met	Asp	
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Leu	Asn	Asn	Gln	Glu	Tyr	Thr	Ile	Thr	Gly	Asp	Leu	Asp	Ser	Leu	Asn	
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atc	agc	ccg	gat	tcc	aac	acc	cct	acc	cta	tta	gtt	tta	agc	gct	tta	296
Ile	Ser	Pro	Asp	Ser	Asn	Thr	Pro	Thr	Leu	Leu	Val	Leu	Ser	Ala	Leu	
			70					75					80			
gat	aat	tct	tta	aaa	gat	tac	gcc	ccc	agc	ttt	aac	atc	tta	aaa	aaa	344
Asp	Asn	Ser	Leu	Lys	Asp	Tyr	Ala	Pro	Ser	Phe	Asn	Ile	Leu	Lys	Lys	
		85					90					95				
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Thr	Phe	Lys	Asp	Arg	Leu	Arg	Val	Leu	Ile	Leu	Leu	Asn	Lys	Pro	Tyr	
	100					105					110					
tca	agc	gat	gca	atc	aaa	gac	ttt	agc	gcg	cat	ttt	caa	gct	gat	ttg	440
Ser	Ser	Asp	Ala	Ile	Lys	Asp	Phe	Ser	Ala	His	Phe	Gln	Ala	Asp	Leu	
115					120				125						130	
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Met	Ile	Leu	Asn	Pro	Lys	Asp	Thr	Ala	Leu	Phe	Asp	His	Leu	Lys	Tyr	
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gac	gct	tta	aac	cat	tct	ttt	aac	atg	ctc	tta	tac	cac	aaa	cac	caa	536
Asp	Ala	Leu	Asn	His	Ser	Phe	Asn	Met	Leu	Leu	Tyr	His	Lys	His	Gln	
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 50 55 60
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 65 70 75 80
 Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu
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 Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys
 100 105 110
 Pro Tyr Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala
 115 120 125
 Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu
 130 135 140
 Lys Tyr Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys
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35	40	45	50
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Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu Pro Ser			
	55	60	65
cct cgc ctt gag aat aac gat cag ccc gtc att agt tct aac ccc act			296
Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn Pro Thr			
	70	75	80
aac gct atc cct aac acc ccc att ctc acg cct aat aat gtc att gaa			344
Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val Ile Glu			
	85	90	95
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100	105	110	
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Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro			
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Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu			
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Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn			
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Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val			
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Ala Lys Leu Glu Lys Ala Ala Leu Met Asn Gly Val Tyr Ile Ser Pro	
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Tyr Lys Lys Ser Thr His Cys Gln Arg Thr His Leu Glu Asn Lys Ser	
245 250 255	
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Pro Phe Ile Asp Ala Asp Lys Met Ala Met Gln Ser Ala Gly Leu Leu	
275 280 285 290	
aga aag aat aaa ggt gtc ttg att gct ttt gct aca gat att tgc atg	968
Arg Lys Asn Lys Gly Val Leu Ile Ala Phe Ala Thr Asp Ile Cys Met	
295 300 305	
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Glu Arg Asn Glu His Lys Lys Glu Glu Phe Ile Ser Leu Lys Asp Ser	
310 315 320	
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Cys Thr Gln Ser Gln Ala Lys Ile Tyr Asn Asn Lys Glu Arg Phe Asp	
325 330 335	
aaa ttc ata caa gat tac caa aaa gac tta aaa act tgt ctt tta gac	1112
Lys Phe Ile Gln Asp Tyr Gln Lys Asp Leu Lys Thr Cys Leu Leu Asp	
340 345 350	
act tct aac act aaa gaa gaa gtg gag caa aat ttt tca caa tgc caa	1160
Thr Ser Asn Thr Lys Glu Glu Val Glu Gln Asn Phe Ser Gln Cys Gln	
355 360 365 370	
aaa gag caa ttg aga gat gat aac aaa ggc ttg ggt ttc act tta gaa	1208
Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr Leu Glu	
375 380 385	
gaa ttg gtt aaa aaa tac gct aag taaagttatt taattttatg gatgggtttta	1262
Glu Leu Val Lys Lys Tyr Ala Lys	
390	

aaaatccatt ccatagttat tgt

1285

<210> 44

<211> 394

<212> PRT

<213> Helicobacter pylori

<400> 44

Met	Lys	Glu	Thr	Arg	Leu	Leu	Lys	Leu	Arg	Ala	Leu	Ser	Leu	Ala	Cys
1				5					10					15	
Leu	Met	Gly	Leu	Gly	Val	Ser	Gly	Cys	Ala	Phe	Leu	Asp	Lys	Gln	Ile
		20						25					30		
Leu	Asn	Asp	His	Leu	Thr	Lys	Ala	Lys	Asn	Asn	Pro	Lys	Tyr	Asp	Cys
		35					40					45			
Gln	Lys	Glu	Met	Trp	Ser	Phe	Pro	Lys	Lys	Tyr	Asp	Gly	Ile	Asn	Gln
	50					55					60				
Cys	Leu	Lys	Ala	Gln	Glu	Glu	Leu	Ile	Glu	Pro	Ile	Ile	Thr	Lys	Lys
65					70				75						80
Ile	Asp	Gln	Tyr	Gln	Cys	Asp	Asp	Phe	Thr	Asn	Glu	Gly	Leu	Lys	Asp
				85					90					95	
Lys	Cys	Phe	Lys	Arg	Asn	Asp	Ala	Tyr	Leu	Asn	Thr	Leu	Leu	Thr	Pro
			100					105					110		
Ile	Ile	Gln	Lys	Gln	Glu	Arg	Arg	Phe	Ser	Cys	Ser	Asp	Phe	His	Asn
		115					120					125			
Pro	Glu	Leu	Lys	Glu	Gln	Cys	Met	Asp	Lys	Thr	Asn	Ala	Tyr	Glu	Lys
	130					135					140				
Gln	Lys	Asp	Arg	Gln	Lys	Arg	Leu	Ile	Asn	Leu	Val	Gln	Leu	Glu	Ala
145					150					155					160
Phe	Glu	Lys	Glu	Tyr	Ala	Gln	Tyr	Lys	Pro	Tyr	Ile	Ile	Pro	Tyr	Phe
				165					170					175	
Thr	Lys	Glu	Cys	Val	Lys	Asn	Ala	Pro	His	Leu	Ala	Asn	Lys	Glu	Arg
			180					185					190		
Leu	Cys	Gln	Lys	Glu	Val	His	Glu	Lys	Phe	Asp	Asp	Pro	Tyr	Ser	Ser
		195					200					205			
Ser	Lys	Glu	Leu	Ser	Val	Gln	Ser	Ala	Ile	Ser	Phe	Cys	Ile	Lys	Lys
	210					215					220				
Val	Asp	Ala	Lys	Leu	Glu	Lys	Ala	Ala	Leu	Met	Asn	Gly	Val	Tyr	Ile
225					230					235					240
Ser	Pro	Tyr	Lys	Lys	Ser	Thr	His	Cys	Gln	Arg	Thr	His	Leu	Glu	Asn
				245					250					255	
Lys	Ser	Leu	Lys	Glu	Ile	Ala	Leu	Asn	Met	Asn	Pro	Lys	Leu	Glu	Lys
			260					265					270		
Gln	Ser	Pro	Phe	Ile	Asp	Ala	Asp	Lys	Met	Ala	Met	Gln	Ser	Ala	Gly
		275					280					285			
Leu	Leu	Arg	Lys	Asn	Lys	Gly	Val	Leu	Ile	Ala	Phe	Ala	Thr	Asp	Ile
	290					295					300				
Cys	Met	Glu	Arg	Asn	Glu	His	Lys	Lys	Glu	Glu	Phe	Ile	Ser	Leu	Lys
305					310					315					320
Asp	Ser	Cys	Thr	Gln	Ser	Gln	Ala	Lys	Ile	Tyr	Asn	Asn	Lys	Glu	Arg
				325					330					335	
Phe	Asp	Lys	Phe	Ile	Gln	Asp	Tyr	Gln	Lys	Asp	Leu	Lys	Thr	Cys	Leu
			340					345					350		
Leu	Asp	Thr	Ser	Asn	Thr	Lys	Glu	Glu	Val	Glu	Gln	Asn	Phe	Ser	Gln
			355				360						365		

Cys Gln Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr
 370 375 380
 Leu Glu Glu Leu Val Lys Lys Tyr Ala Lys
 385 390

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 <211> 835
 <212> DNA
 <213> Helicobacter pylori

<220>
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 ttagagcatg ggcgtttgac aga atg cta agg gtt tta agc gtt ggt gtt gct 113
 Met Leu Arg Val Leu Ser Val Gly Val Ala
 1 5 10
 ttt att tta cta ggg tgt cag ttt ttc aac aaa acg acg ctg cat tta 161
 Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu
 15 20 25
 aaa tat aaa gat tac ccc aaa aat agc gct tta aaa acc gct ttc act 209
 Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr
 30 35 40
 tta acc ccc cct aaa atc ttt ttt aac gcc cgt ttt gtg ccg ccc ttt 257
 Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe
 45 50 55
 tac caa aaa gaa ttt aaa aaa gcg atc acc caa caa atc gct tat ttt 305
 Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe
 60 65 70
 tta aaa gat aaa agt gct ttt att ctc aat gtt tca ggc aat gtt ttt 353
 Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe
 75 80 85 90
 ttt tct ttt gaa gag aat cct aaa gat tta aaa gcc att aaa gaa agg 401
 Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg
 95 100 105
 ctt aaa aag acg att gag cct aac gct gac cca aaa gcc gtc atg cgt 449
 Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg
 110 115 120
 ttt tta aac ctt caa gcg agc ttg att tta gaa tgc gtc ccg caa acc 497
 Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr
 125 130 135
 act tgc ccg ttt gac acc ctt tta atc ccc acc gct ttc agc gtg cct 545
 Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro

140	145	150	
ggt tat tac gct aat cgt ttg ggc gat aac ccc tct ctt ttt tcc caa	593		
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln			
155	160	165	170
gag gat aaa acc tat cat aac gct ttg atc aaa gcc ctt aat aag gct	641		
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala			
175	180	185	
tac tat tct ctt atg gag ggt tta gaa aag cgt ttg aac gct ata aaa	689		
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys			
190	195	200	
aat gca gag tgg ctt taaggcatga aaaagattgc attttttatt tttgtcattt	744		
Asn Ala Glu Trp Leu			
205			
tgtttttcggt agggatttat ttaatttggc atgttttatt ggaaaaagcc ctagaattga	804		
aattagcaac ctcagctaatt gatttgcttt t	835		
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<211> 207			
<212> PRT			
<213> Helicobacter pylori			
<400> 46			
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Gln Phe Phe Asn Lys Thr Thr Leu His Leu Lys Tyr Lys Asp Tyr Pro			
20	25	30	
Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr Leu Thr Pro Pro Lys Ile			
35	40	45	
Phe Phe Asn Ala Arg Phe Val Pro Pro Phe Tyr Gln Lys Glu Phe Lys			
50	55	60	
Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe Leu Lys Asp Lys Ser Ala			
65	70	75	80
Phe Ile Leu Asn Val Ser Gly Asn Val Phe Phe Ser Phe Glu Glu Asn			
85	90	95	
Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg Leu Lys Lys Thr Ile Glu			
100	105	110	
Pro Asn Ala Asp Pro Lys Ala Val Met Arg Phe Leu Asn Leu Gln Ala			
115	120	125	
Ser Leu Ile Leu Glu Cys Val Pro Gln Thr Thr Cys Pro Phe Asp Thr			
130	135	140	
Leu Leu Ile Pro Thr Ala Phe Ser Val Pro Val Tyr Tyr Ala Asn Arg			
145	150	155	160
Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln Glu Asp Lys Thr Tyr His			
165	170	175	
Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala Tyr Tyr Ser Leu Met Glu			
180	185	190	
Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys Asn Ala Glu Trp Leu			
195	200	205	

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<210> 47
<211> 763
<212> DNA
<213> Helicobacter pylori
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aaaaaataac catgagttat tcaaaaatttt aacttttataa gacaggtggc atg cgt																56
Met Arg																
1																
tta	aaa	cat	ttt	aaa	act	ttc	ctt	ttt	atc	aca	atg	gca	atc	att	gta	104
Leu	Lys	His	Phe	Lys	Thr	Phe	Leu	Phe	Ile	Thr	Met	Ala	Ile	Ile	Val	
5						10						15				
ata	ggt	acc	ggt	tgc	gcg	aac	aaa	aag	aaa	aaa	aaa	gac	gaa	tac	aac	152
Ile	Gly	Thr	Gly	Cys	Ala	Asn	Lys	Lys	Lys	Lys	Lys	Asp	Glu	Tyr	Asn	
20						25						30				
aaa	ccg	gcg	atc	ttt	tgg	tat	caa	ggg	att	ttg	aga	gaa	atc	ctt	ttt	200
Lys	Pro	Ala	Ile	Phe	Trp	Tyr	Gln	Gly	Ile	Leu	Arg	Glu	Ile	Leu	Phe	
35			40						45			50				
gct	aat	tta	gaa	aca	gcg	gac	aat	tac	tat	tct	tct	tta	caa	agc	gaa	248
Ala	Asn	Leu	Glu	Thr	Ala	Asp	Asn	Tyr	Tyr	Ser	Ser	Leu	Gln	Ser	Glu	
55							60						65			
cac	atc	aat	tcc	ccc	ctt	gtc	cca	gaa	gcg	atg	cta	gct	tta	ggg	caa	296
His	Ile	Asn	Ser	Pro	Leu	Val	Pro	Glu	Ala	Met	Leu	Ala	Leu	Gly	Gln	
70						75						80				
gcg	cac	atg	aaa	aag	aaa	gag	tat	gtt	tta	gcg	tct	ttt	tac	ttt	gat	344
Ala	His	Met	Lys	Lys	Lys	Glu	Tyr	Val	Leu	Ala	Ser	Phe	Tyr	Phe	Asp	
85						90						95				
gaa	tac	atc	aag	cgc	ttt	ggg	act	aag	gac	aat	gtg	gat	tat	ttg	act	392
Glu	Tyr	Ile	Lys	Arg	Phe	Gly	Thr	Lys	Asp	Asn	Val	Asp	Tyr	Leu	Thr	
100						105						110				
ttt	tta	aaa	ttg	caa	tcg	cat	tat	tac	gct	ttc	aaa	aac	cat	tct	aaa	440
Phe	Leu	Lys	Leu	Gln	Ser	His	Tyr	Tyr	Ala	Phe	Lys	Asn	His	Ser	Lys	
115			120						125						130	
gac	cag	gaa	ttt	atc	tct	aat	tct	att	gtg	agt	tta	ggc	gaa	ttt	ata	488
Asp	Gln	Glu	Phe	Ile	Ser	Asn	Ser	Ile	Val	Ser	Leu	Gly	Glu	Phe	Ile	
135							140						145			
gaa	aaa	tac	cct	aac	agc	cgt	tac	cgc	ccc	tat	gta	gaa	tac	atg	caa	536
Glu	Lys	Tyr	Pro	Asn	Ser	Arg	Tyr	Arg	Pro	Tyr	Val	Glu	Tyr	Met	Gln	
150						155						160				
atc	aaa	ttc	att	tta	ggg	caa	aat	gag	ctc	aat	cgc	gcg	atc	gcg	aat	584

Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn
165 170 175

gtc tat aaa aaa cgc cac aag cct gag ggc gtg aaa cgc tat tta gaa 632
Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu
180 185 190

agg ata gat gag act tta gaa aaa gag act aaa ccc aaa cca tcg cac 680
Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His
195 200 205 210

atg cct tgg tat gtg tta att ttt gat tgg taggatattt caaaaccata 730
Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
215 220

cacattataa cagagagatg aaaaatgact gaa 763

<210> 48
<211> 220
<212> PRT
<213> Helicobacter pylori

<400> 48
Met Arg Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile
1 5 10 15
Ile Val Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu
20 25 30
Tyr Asn Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile
35 40 45
Leu Phe Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln
50 55 60
Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu
65 70 75 80
Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr
85 90 95
Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr
100 105 110
Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His
115 120 125
Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu
130 135 140
Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr
145 150 155 160
Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile
165 170 175
Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr
180 185 190
Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro
195 200 205
Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
210 215 220

<210> 49
<211> 801

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (75)...(749)

<400> 49

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gaaaaaggct ctgctttgat agataaattt gacgctaacc cctataaaac gattttttgga 60
gaaaggaaat aatc atg aga gct acg gcg ata aaa atc ttt tca ctc tca 110
          Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser
                1             5             10
```

```
tca gca tta gcc cta ttg ctt cat ggt tgc ttg agc atc aat tta aaa 158
Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys
          15             20             25
```

```
caa atg cta cca gag atc aga act tac gat ttg aat gcg agt tct ttt 206
Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe
          30             35             40
```

```
gaa atc acg caa tgc gct aaa cct ttg act gaa gtg agg ctc att agt 254
Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser
          45             50             55             60
```

```
att ttg agc gcg gat tta ttc aac act aaa gag atc gtt ttt aaa gcc 302
Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala
          65             70             75
```

```
aaa gac ggg cag atc acg cat ggg aag cac caa aaa tgg ata gac ttg 350
Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu
          80             85             90
```

```
cct cgc aac atg cta aaa acc atg ttc atg caa gaa gcg caa aaa gca 398
Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala
          95             100             105
```

```
tgc tta ggc gtg gct ttg cct cct tat ggc gcg ggt gca ccc act tat 446
Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr
          110             115             120
```

```
gcg gtt cgt ttt acg att tta tcg ttt tct ctt tta gaa aaa gaa aat 494
Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn
          125             130             135             140
```

```
tct acc tat agg gcg gaa ttt gca cta ggc tat gac att agc gtg aaa 542
Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys
          145             150             155
```

```
ggc gat tcg cat tct ggg gtg atc att aag cat gaa aat att tct agc 590
Gly Asp Ser His Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser
          160             165             170
```

```
ttg gaa aat aaa acg acc aaa acg agt aaa aat ggc aat caa gat ttt 638
Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe
```

175	180	185	
caa gaa agc gcg ata caa tct ctc caa cat gta agc gtg caa gcg att			686
Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile			
190	195	200	
caa gaa gcg gtt tct ttg att aaa aaa gcc att gaa gcg caa agc gta			734
Gln Glu Ala Val Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val			
205	210	215	220
agc ccg tta aaa aaa taaaaaataa ggaggaattg tttgatttta cgattggctg			789
Ser Pro Leu Lys Lys			
225			
gagcaagcgt tt			801

<210> 50
 <211> 225
 <212> PRT
 <213> Helicobacter pylori

<400> 50

Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser Ser Ala Leu Ala			
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Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro			
20	25	30	
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Ile Thr Gln			
35	40	45	
Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala			
50	55	60	
Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala Lys Asp Gly Gln			
65	70	75	80
Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu Pro Arg Asn Met			
85	90	95	
Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala Cys Leu Gly Val			
100	105	110	
Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr Ala Val Arg Phe			
115	120	125	
Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn Ser Thr Tyr Arg			
130	135	140	
Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys Gly Asp Ser His			
145	150	155	160
Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser Leu Glu Asn Lys			
165	170	175	
Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe Gln Glu Ser Ala			
180	185	190	
Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile Gln Glu Ala Val			
195	200	205	
Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val Ser Pro Leu Lys			
210	215	220	
Lys			
225			

<210> 51

Leu	Phe	Ser	Ala	Cys	Lys	Asp	Glu	Pro	Lys	Lys	Ser	Ser	Gln	Ser	His
			20					25					30		
Gln	Asn	Asn	Thr	Lys	Ile	Thr	Lys	Asn	Asn	Pro	Ile	Asn	Gln	Ala	Asn
	35						40					45			
Asn	Asp	Ile	Arg	Lys	Ile	Glu	His	Glu	Glu	Glu	Asp	Glu	Lys	Ala	Thr
	50					55					60				
Lys	Glu	Val	Asn	Asp	Leu	Ile	Asn	Asn	Glu	Asn	Lys	Ile	Asp	Glu	Ile
65					70				75						80
Asn	Asn	Glu	Glu	Asn	Ala	Asp	Pro	Ser	Gln	Lys	Arg	Thr	Asn	Asn	Val
			85						90				95		
Leu	Gln	Arg	Ala	Thr	Asn	His	Gln	Asp	Asn	Leu	Asn	Ser	Pro	Leu	Asn
			100					105					110		
Arg	Lys	Tyr													
			115												

<210> 53
 <211> 1121
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (121)...(1065)

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 atg ggt ttg gcg ttg gaa aaa gtt tgt ttt tta ggc gtt att ttt ttg 168
 Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
 1 5 10 15

att agc gct tgc acg gtt aaa aaa gag ggg gta aag aat ttg tct tac 216
 Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
 20 25 30

aag cat gaa agc ttg cgc gct tat gaa aac gct aaa gat tat gat ccg 264
 Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
 35 40 45

aca acc aaa aaa gcc gcc tat aaa cgc aat ttt ttt gaa cgc cat ttc 312
 Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
 50 55 60

aaa cgc tac tcc gat tcg caa gat agc aac aca aaa gat cag cca cta 360
 Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
 65 70 75 80

gat aac ggc atg cgc gat tct agc tcg atc caa aga gcc acc atg cgc 408
 Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
 85 90 95

cct tat caa gtg ggg ggc aag tgg tat tac ccc act aaa gtg gat tta 456
 Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
 100 105 110

ggc gaa aaa ttt gat ggc gtt gcg agt tgg tat ggc cct aac ttc cat	504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His	
115 120 125	
gcc aaa aaa acc agt aat ggg gaa att tat aac atg tat gcc cac acc	552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr	
130 135 140	
gcc gcg cac aaa act tta ccc atg aac acc gtg gtg aaa gtc atc aat	600
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn	
145 150 155 160	
gtt gat aat aac tta agc acc att gtg cgc atc aac gat aga ggg cct	648
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro	
165 170 175	
ttt gtg agc gat cgc atc att gat ttg tct aat gcg gcc gct agg gat	696
Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp	
180 185 190	
att gac atg gtt aaa aaa ggc aca gcc agc gtg cgt ctc att gtt ttg	744
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu	
195 200 205	
ggc ttt ggt ggg gtt atc tcc acg caa tac gaa caa tcc ttt aac gcc	792
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala	
210 215 220	
agc tct tca aag atc ttg cac aag gaa ttt aaa gtc ggc gag agc gaa	840
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu	
225 230 235 240	
aaa agc gtg agc gga ggg aaa ttt tct ttg caa atg ggg gct ttt aga	888
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg	
245 250 255	
aac caa ata ggt gct caa act tta gcg gat aaa ttg caa gca gaa aat	936
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn	
260 265 270	
cca aat tac agc gtc aag gtt gct ttt aaa gac gat ttg tat aaa gtt	984
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val	
275 280 285	
tta gtt caa ggg ttt caa agc gaa gaa gag gct agg gat ttt atg aaa	1032
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys	
290 295 300	
aaa tac aac cag aat gcg gtt tta acg aga gaa tgattaagtt attgctttta	1085
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu	
305 310 315	
gatgtggatg gcacgctcac agacggatcg ttgtat	1121

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 <213> Helicobacter pylori

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 20 25 30
 Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
 35 40 45
 Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
 50 55 60
 Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
 65 70 75 80
 Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
 85 90 95
 Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
 100 105 110
 Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
 115 120 125
 Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
 130 135 140
 Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
 145 150 155 160
 Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
 165 170 175
 Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp
 180 185 190
 Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu
 195 200 205
 Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala
 210 215 220
 Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu
 225 230 235 240
 Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg
 245 250 255
 Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn
 260 265 270
 Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val
 275 280 285
 Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys
 290 295 300
 Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu
 305 310 315

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 <213> Helicobacter pylori

<220>
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<222> (51)...(761)

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Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys Ala Ser	
5 10 15	
tat aag atc acg cct gaa cat gtt act tcc tat aat aat ggg att caa	152
Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly Ile Gln	
20 25 30	
gtg atg act tcc acg caa gcc aaa tct aaa gtc cag cta gaa atc gct	200
Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu Ile Ala	
35 40 45 50	
caa agc aag ttg aaa ggc ttg aac gag tcc ccc tta gtg ctg tat gta	248
Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu Tyr Val	
55 60 65	
gcg gcg caa gtt ata gag gga agt cct gtg gtg ttt agc cgt aaa gcc	296
Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg Lys Ala	
70 75 80	
att tca gtg tct atc aac caa acg aat tta ccg gtc tta agc ctg aga	344
Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser Leu Arg	
85 90 95	
cag gtg atg aaa tcc agt ttt gat ttt gag ggt att tta caa agt ttt	392
Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln Ser Phe	
100 105 110	
aat atc gcc gtg ccg acc acc cct att gat aat gtc aat atg atc acc	440
Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met Ile Thr	
115 120 125 130	
ccg cct atg ttt tat tac ggg caa ggg gga ttt tta gct tat aac ggc	488
Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr Asn Gly	
135 140 145	
atg atg tat ggg gga atg ggc atg tat ggg cca ggc ttt ggc atg atg	536
Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly Met Met	
150 155 160	
atg atg gat gat gta gaa gag caa gaa gtc atg caa gaa agc cgc caa	584
Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser Arg Gln	
165 170 175	
gct tta aaa atc cta gcg atc aat tac ctt aaa aac aac acc ctt aat	632
Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr Leu Asn	
180 185 190	

gtt gag agt aag gct aag gga ggg ttt gtg gtg gtg gat acc aaa aac 680
 Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr Lys Asn
 195 200 205 210

ctt aaa acc ccg ggt gtg gtg gtg gtt aaa gtc ttt tta gaa gat gaa 728
 Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu Asp Glu
 215 220 225

atc cac acc ttt aaa att gat att tct aag atg taatcgcccc ctttaataaa 781
 Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met
 230 235

agcctttggg ccattccacct aaaggttttt 811

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 <213> Helicobacter pylori

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 35 40 45
 Ile Ala Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu
 50 55 60
 Tyr Val Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg
 65 70 75 80
 Lys Ala Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser
 85 90 95
 Leu Arg Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln
 100 105 110
 Ser Phe Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met
 115 120 125
 Ile Thr Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr
 130 135 140
 Asn Gly Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly
 145 150 155 160
 Met Met Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser
 165 170 175
 Arg Gln Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr
 180 185 190
 Leu Asn Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr
 195 200 205
 Lys Asn Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu
 210 215 220
 Asp Glu Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met
 225 230 235

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<213> Helicobacter pylori

<220>

<221> CDS

<222> (97)...(1371)

<400> 57

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tactactaaaa caatctcaag gtttcaaaat ttagcc atg cgt ctt ctt ctg ttc 114
                                     Met Arg Leu Leu Leu Phe
                                     1                               5

aat caa aac gct ttt tta tta gcg tgc atg ttt gtt tca agc gtg tat 162
Asn Gln Asn Ala Phe Leu Leu Ala Cys Met Phe Val Ser Ser Val Tyr
          10                               15                               20

gtg aac gct gtc tta gac gct tat gca att gaa aac ccc tat att tct 210
Val Asn Ala Val Leu Asp Ala Tyr Ala Ile Glu Asn Pro Tyr Ile Ser
          25                               30                               35

atc aca ctc aca agc cta tta gcc cct tta agc atg cta gcg ttt tta 258
Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu Ser Met Leu Ala Phe Leu
          40                               45                               50

aaa acc cct aga aat agt gct ttt gct ttg ggg ttt ttt gtg ggg gcg 306
Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly Phe Phe Val Gly Ala
          55                               60                               65                               70

tta ttg ttt tat tgg tgc gct tta agc ttt cgc tac tcg gat ttc act 354
Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe Arg Tyr Ser Asp Phe Thr
          75                               80                               85

tat tta ttg ccc tta atc att gtt tta ata gcg tta gtt tat ggg gtt 402
Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile Ala Leu Val Tyr Gly Val
          90                               95                               100

tta ttt tat ttg ttg ctc tat ttt gaa aac ccc tat ttc agg ctt ttg 450
Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro Tyr Phe Arg Leu Leu
          105                               110                               115

agt ttt tta ggc tct agt ttt atc cac ccc ttt gga ttt gat tgg tta 498
Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe Gly Phe Asp Trp Leu
          120                               125                               130

gtc cca gat agc ttt ttt tct tat agc gtg ttt aga gtg gat aaa tta 546
Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe Arg Val Asp Lys Leu
          135                               140                               145                               150

tcg cta ggg ctt gtt ttt ttg gct tgc att ttt ttg agc act aaa cca 594
Ser Leu Gly Leu Val Phe Leu Ala Cys Ile Phe Leu Ser Thr Lys Pro
          155                               160                               165

ttg aaa aaa tat agg atc ata ggg gtt tta ttg tta ctt ggc gcg ttg 642
Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu Leu Leu Leu Gly Ala Leu
          170                               175                               180
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gat ttt aat ggt ttc aaa aca agc gat tta aaa aag gtt gga aat att	690
Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu Lys Lys Val Gly Asn Ile	
185 190 195	
gaa tta gtc tct aca aaa acg ccc caa gat ttg aaa ttt gac tca agt	738
Glu Leu Val Ser Thr Lys Thr Pro Gln Asp Leu Lys Phe Asp Ser Ser	
200 205 210	
tac ctt aat gat att gaa aac aac att ctt aaa gaa atc aag ctc gct	786
Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu Lys Glu Ile Lys Leu Ala	
215 220 225 230	
caa agc aag caa aaa acc ttg att gtt ttt cca gaa acc gcc tac ccc	834
Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro Glu Thr Ala Tyr Pro	
235 240 245	
atc gct tta gaa aac tcc ccc ttt aaa gcg aag cta gaa gat tta agc	882
Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala Lys Leu Glu Asp Leu Ser	
250 255 260	
gat aat att gct att tta ata ggg aca tta cgg act caa ggc tat aat	930
Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu Arg Thr Gln Gly Tyr Asn	
265 270 275	
ctt tat aac agc tcg ttt tta ttt tct aaa gaa agc gtt cag atc gct	978
Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Glu Ser Val Gln Ile Ala	
280 285 290	
gat aaa gta att tta gcc ccc ttt ggc gag acc atg cct tta ccg gaa	1026
Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Thr Met Pro Leu Pro Glu	
295 300 305 310	
ttt ctt caa aaa ccc ctt gaa aag ctc ttt ttt ggc gag agc act tat	1074
Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe Gly Glu Ser Thr Tyr	
315 320 325	
tta tac cgc aat gct cct cat ttc agc gat ttt aca tta gac gat ttt	1122
Leu Tyr Arg Asn Ala Pro His Phe Ser Asp Phe Thr Leu Asp Asp Phe	
330 335 340	
act ttt cgc ccc ctg att tgc tat gaa ggc act tcc aaa ccc gct tat	1170
Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly Thr Ser Lys Pro Ala Tyr	
345 350 355	
tca aac agc cct tca aaa att ttt atc gtg atg agc aat aac gca tgg	1218
Ser Asn Ser Pro Ser Lys Ile Phe Ile Val Met Ser Asn Asn Ala Trp	
360 365 370	
ttt agc cca agc att gaa ccc acc tta caa aga acg ctt tta aaa tac	1266
Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln Arg Thr Leu Leu Lys Tyr	
375 380 385 390	
tac gca agg cgt tat gat aag atc atc ttg cac agc gcg aac ttt tca	1314
Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu His Ser Ala Asn Phe Ser	

395	400	405	
act tct tac atc tta agc cct agt tta tta ggc gat att ctt ttt agg			1362
Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu Gly Asp Ile Leu Phe Arg			
410	415	420	
aaa cga tca tgattaaagc gattaatatt tctcatgctt ttgaaaagcc			1411
Lys Arg Ser			
425			
tctttataat ggcg			1425
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<213> Helicobacter pylori			
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Phe Val Ser Ser Val Tyr Val Asn Ala Val Leu Asp Ala Tyr Ala Ile			
20	25	30	
Glu Asn Pro Tyr Ile Ser Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu			
35	40	45	
Ser Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu			
50	55	60	
Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe			
65	70	75	80
Arg Tyr Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile			
85	90	95	
Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn			
100	105	110	
Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro			
115	120	125	
Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val			
130	135	140	
Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Val Phe Leu Ala Cys Ile			
145	150	155	160
Phe Leu Ser Thr Lys Pro Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu			
165	170	175	
Leu Leu Leu Gly Ala Leu Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu			
180	185	190	
Lys Lys Val Gly Asn Ile Glu Leu Val Ser Thr Lys Thr Pro Gln Asp			
195	200	205	
Leu Lys Phe Asp Ser Ser Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu			
210	215	220	
Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe			
225	230	235	240
Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala			
245	250	255	
Lys Leu Glu Asp Leu Ser Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu			
260	265	270	
Arg Thr Gln Gly Tyr Asn Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys			
275	280	285	
Glu Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu			

290	295	300
Thr Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe		
305	310	315
Phe Gly Glu Ser Thr Tyr Leu Tyr Arg Asn Ala Pro His Phe Ser Asp		320
	325	330
Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly		335
	340	345
Thr Ser Lys Pro Ala Tyr Ser Asn Ser Pro Ser Lys Ile Phe Ile Val		350
	355	360
Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln		365
	370	375
Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu		380
385	390	395
His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu		400
	405	410
Gly Asp Ile Leu Phe Arg Lys Arg Ser		415
	420	425

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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(713)

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Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Leu Ile	
5	10
15	
tcg ctg ttt tta agc gct tgc aaa tcc aac aat aaa gac aag tta gac	152
Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp	
20	25
30	
gaa aat ctt tta agc tct ggc tct caa agc tcc aaa gaa tta aac gat	200
Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp	
35	40
45	50
gag cga gac aat ata gac aaa aag agt tac gct ggt tta gaa gat gtt	248
Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val	
55	60
65	
ttt tca gac aat aag tcc att agt cct aac gat aaa tac atg ctt tta	296
Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu	
70	75
80	
gtt ttt ggc cgt aat ggt tgc tcc tat tgc gaa agg ttt aaa aaa gat	344
Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp	

85	90	95	
ctc aaa aat gtc aaa gaa ttg cgc gac tac att aaa gag cat ttt agc			392
Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser			
100	105	110	
gct tac tat gtc aat atc agc tac tcc aaa gag cat gat ttt aaa gtc			440
Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val			
115	120	125	130
ggc gat aaa aat aat gaa aaa gaa atc aaa atg tcc aca gaa gaa tta			488
Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu			
	135	140	145
gcg caa att tat gcc gtc caa tcc acc cct acg att gtt tta tcc gat			536
Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp			
	150	155	160
aaa acc ggc aaa acc atc tat gaa ttg ccc ggc tat atg ccc tct acg			584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr			
	165	170	175
caa ttt tta gcc gtg tta gaa ttt atc ggc gat ggg aag tat caa gac			632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp			
	180	185	190
aca aaa gac gat gag gat ctc act aaa aaa tta aag gct tac atc aag			680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys			
	195	200	205
tat aaa acc aac ctt tct aaa agc aag tct aac taggaaagcc taatgaagaa			733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn			
	215	220	
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	20	25	30
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu			
	35	40	45
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu			
	50	55	60
Asp Val Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met			
	65	70	75
Leu Leu Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys			
	85	90	95
Lys Asp Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His			

		100						105					110				
Phe	Ser	Ala	Tyr	Tyr	Val	Asn	Ile	Ser	Tyr	Ser	Lys	Glu	His	Asp	Phe		
		115						120				125					
Lys	Val	Gly	Asp	Lys	Asn	Asn	Glu	Lys	Glu	Ile	Lys	Met	Ser	Thr	Glu		
		130					135					140					
Glu	Leu	Ala	Gln	Ile	Tyr	Ala	Val	Gln	Ser	Thr	Pro	Thr	Ile	Val	Leu		
145					150				155					160			
Ser	Asp	Lys	Thr	Gly	Lys	Thr	Ile	Tyr	Glu	Leu	Pro	Gly	Tyr	Met	Pro		
			165					170					175				
Ser	Thr	Gln	Phe	Leu	Ala	Val	Leu	Glu	Phe	Ile	Gly	Asp	Gly	Lys	Tyr		
		180					185					190					
Gln	Asp	Thr	Lys	Asp	Asp	Glu	Asp	Leu	Thr	Lys	Lys	Leu	Lys	Ala	Tyr		
		195					200					205					
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<220>
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Met Arg
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Leu	Leu	Phe	Leu	Leu	Leu	Ser	Ala	Ala	Phe	Met	Leu	Leu	Ala	Glu	Glu	
		5					10					15				

aaa	ata	tct	tta	aac	gat	gac	gcc	ccc	att	aaa	cta	gtg	cat	tgg	caa	154
Lys	Ile	Ser	Leu	Asn	Asp	Asp	Ala	Pro	Ile	Lys	Leu	Val	His	Trp	Gln	
	20					25					30					

aat	gca	tta	aaa	gaa	gtc	caa	cct	gat	tca	aac	gct	cca	gca	aca	cca	202
Asn	Ala	Leu	Lys	Glu	Val	Gln	Pro	Asp	Ser	Asn	Ala	Pro	Ala	Thr	Pro	
	35				40					45					50	

cct	ata	aaa	gcc	gtg	caa	acc	acg	ctc	act	ttt	gaa	acg	cct	ttt	aac	250
Pro	Ile	Lys	Ala	Val	Gln	Thr	Thr	Leu	Thr	Phe	Glu	Thr	Pro	Phe	Asn	
			55					60						65		

aaa	acg	cct	aaa	atc	atg	gaa	gtt	gaa	ggg	caa	aag	gtg	atc	gtc	tta	298
Lys	Thr	Pro	Lys	Ile	Met	Glu	Val	Glu	Gly	Gln	Lys	Val	Ile	Val	Leu	
		70					75					80				

aaa	aac	gct	aaa	ctg	gat	tct	aaa	aaa	acc	atg	gat	ttt	aaa	gaa	gcc	346
Lys	Asn	Ala	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Met	Asp	Phe	Lys	Glu	Ala	
		85					90					95				

tct ttg aat gct tta gaa atg ttt tcc tac caa aat gac atc tac ctc	394
Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile Tyr Leu	
100 105 110	
ttg tct aaa aaa gct aaa gtg gaa tta gaa atc caa gct tca aac agc	442
Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser Asn Ser	
115 120 125 130	
aag gat aaa aaa cgg ctc cgc ttt ctc ttt tta ccc aaa ggt ttt cat	490
Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly Phe His	
135 140 145	
tta gcc cca ccg cct aac ctg aaa gaa aaa tct cag caa act aac ctt	538
Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr Asn Leu	
150 155 160	
gca caa aaa gac acc aac gag caa ccc caa agc cct tta aac act cta	586
Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn Thr Leu	
165 170 175	
gag tta aaa ccc cca cta aat tta agc cat gct tat aag gcg cta gcg	634
Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala Leu Ala	
180 185 190	
gtt att gct gcc tta ctc tta ata ttg tat gtc atc aaa aaa aaa att	682
Val Ile Ala Ala Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys Lys Ile	
195 200 205 210	
gtt ccc aca caa ggg tct ttt tct gca aaa gat ttt aag tta gaa att	730
Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu Glu Ile	
215 220 225	
agc gtt ttg ggt cgt gtt gat gcg aac cat aaa atc att tca ata gaa	778
Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser Ile Glu	
230 235 240	
acc aat aag gag cgt tac ttg gtc tta cta agc gat aaa tac ggc ctg	826
Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr Gly Leu	
245 250 255	
ctt tta gac aaa ata agc cca aaa aca tct aaa gaa gaa ctg att aaa	874
Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu Ile Lys	
260 265 270	
gaa gct gaa aat aat ata aag aat tca aaa tta gga aat tta tat gcc	922
Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu Tyr Ala	
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Gly Lys Phe	
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 Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala
 35 40 45
 Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro
 50 55 60
 Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile
 65 70 75 80
 Val Leu Lys Asn Ala Lys Leu Asp Ser Lys Lys Thr Met Asp Phe Lys
 85 90 95
 Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile
 100 105 110
 Tyr Leu Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser
 115 120 125
 Asn Ser Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly
 130 135 140
 Phe His Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr
 145 150 155 160
 Asn Leu Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn
 165 170 175
 Thr Leu Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala
 180 185 190
 Leu Ala Val Ile Ala Ala Leu Leu Ile Leu Tyr Val Ile Lys Lys
 195 200 205
 Lys Ile Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu
 210 215 220
 Glu Ile Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser
 225 230 235 240
 Ile Glu Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr
 245 250 255
 Gly Leu Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu
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 Tyr Ala Gly Lys Phe
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<400> 63

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      Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu
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atc gct tca aga cta atc gtt gta atc cta tat gct ttt atc ttt att 159
Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile
  15             20             25             30

gtt ctc tct ttt tat atg ctc aat atc atc act att ctt aat ttt aaa 207
Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys
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gcg ctt att ttg ggg ttt gtt agt gtt ttt tca agc gca ttg ttt tgt 255
Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys
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ttt tgc ttg gca att ttt gta gct aga att ttt caa aac gaa caa agc 303
Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser
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atc tta gga ttt tgt aat atc atc aat ctc tat gcg cta atg tct tgt 351
Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys
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aat gtt ttt gtt cct tta gaa tac cta cct agt att ggt caa tta ttt 399
Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe
  95             100             105             110

atc aaa aca tct att ttt tac tac ctt aat caa ctt cta atc aaa gct 447
Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala
              115             120             125

ttt caa ggg att gat act ata ctg gtt tta gca act tca aca ttt ttc 495
Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe
              130             135             140

att att ggt ggc att att tta ttt tta cta agc gct aat cgc atg tta 543
Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu
              145             150             155

cta aca cca aaa gaa cgc atg cgt taaaggctta gtcccacccat tgatttattt 597
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Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro Glu Val Asp	
85 90 95	
att ttt acc ggc gtg ggg gat tat gac aag atc gat ata atg att gct	394
Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile Met Ile Ala	
100 105 110 115	
aaa aaa caa aac cag ttc agc gag caa gtg ttt tta agc gag cat tac	442
Lys Lys Gln Asn Gln Phe Ser Glu Gln Val Phe Leu Ser Glu His Tyr	
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aac gca cgc atc atc acg gga tgc agc gtg cat gcg tat gtg aaa att	490
Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr Val Lys Ile	
135 140 145	
tct gag ggt tgc aat caa aaa tgt tct ttt tgc gct atc cct agc ttt	538
Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile Pro Ser Phe	
150 155 160	
aag ggg aaa ttg caa agc agg gaa ttg gac tcc att tta aaa gaa gtg	586
Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu Lys Glu Val	
165 170 175	
gaa aat ctc gcg ctt aaa ggc tat acg gat atg act ttt atc gct caa	634
Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe Ile Ala Gln	
180 185 190 195	
gac tct agc tcc ttt tta tac gat aag ggg caa aaa gac ggc ttg atc	682
Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp Gly Leu Ile	
200 205 210	
cag ctc att aga gcg att gat aaa cag caa gcc tta aag agc gcg cgt	730
Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys Ser Ala Arg	
215 220 225	
att tta tat ctc tac ccc tct agc acc acg cta gag ctt att ggc gcg	778
Ile Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu Ile Gly Ala	
230 235 240	
att gaa agt tgc ccc att ttt caa aat tat ttt gac atg ccc atc cag	826
Ile Glu Ser Ser Pro Ile Phe Gln Asn Tyr Phe Asp Met Pro Ile Gln	
245 250 255	
cac atc agc gac tcc atg ctc aaa aag atg cgg cgc aac tct agc caa	874
His Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn Ser Ser Gln	
260 265 270 275	
gcg cac cat tta aag ctt tta gat gcc atg aag cag gtt aaa gaa agc	922
Ala His His Leu Lys Leu Leu Asp Ala Met Lys Gln Val Lys Glu Ser	
280 285 290	
ttt atc aga agc acg atc att gta ggg cat ccg gaa gaa aat gag agc	970
Phe Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu Asn Glu Ser	

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Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln Phe Asp Arg			
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ttg aat att ttt gct ttc agc gct gaa gaa aac acg cat gcc tat tct			1066
Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His Ala Tyr Ser			
325	330	335	
tta gaa aaa gtg cct aaa aaa acc atc aac gct cgc atc aaa gcc ttg			1114
Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile Lys Ala Leu			
340	345	350	355
aat aaa atc gct tta aag cac caa aac cat tcc ttt aag gct ttg ttg			1162
Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys Ala Leu Leu			
360	365	370	
aat aag ccc att aag gcg tta gtg gaa aat aaa gag ggc gag tat ttt			1210
Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly Glu Tyr Phe			
375	380	385	
tac aaa gca agg gat ctc aga tgg gcg cct gaa gtg gat ggg gaa atc			1258
Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp Gly Glu Ile			
390	395	400	
ttg atc aat gat agc gaa cta acc acc ccc tta aaa ccc ggg cat tat			1306
Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro Gly His Tyr			
405	410	415	
acg att gca cct agc gaa ttt aaa gat aat atc cta ctc gct aag gtt			1354
Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu Ala Lys Val			
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Leu Ser Pro Phe			

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 35 40 45
 Thr Cys Gly Phe Ile Glu Ser Ala Lys Gln Glu Ser Ile Gln Thr Ile
 50 55 60
 Leu Asn Ala Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser
 65 70 75 80

Gly	Cys	Leu	Ser	Glu	Arg	Tyr	Lys	Asp	Glu	Ile	Lys	Glu	Leu	Ile	Pro	
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Glu	Val	Asp	Ile	Phe	Thr	Gly	Val	Gly	Asp	Tyr	Asp	Lys	Ile	Asp	Ile	
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Met	Ile	Ala	Lys	Lys	Gln	Asn	Gln	Phe	Ser	Glu	Gln	Val	Phe	Leu	Ser	
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Glu	His	Tyr	Asn	Ala	Arg	Ile	Ile	Thr	Gly	Ser	Ser	Val	His	Ala	Tyr	
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Val	Lys	Ile	Ser	Glu	Gly	Cys	Asn	Gln	Lys	Cys	Ser	Phe	Cys	Ala	Ile	
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Pro	Ser	Phe	Lys	Gly	Lys	Leu	Gln	Ser	Arg	Glu	Leu	Asp	Ser	Ile	Leu	
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Lys	Glu	Val	Glu	Asn	Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asp	Met	Thr	Phe	
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Ile	Ala	Gln	Asp	Ser	Ser	Ser	Phe	Leu	Tyr	Asp	Lys	Gly	Gln	Lys	Asp	
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Gly	Leu	Ile	Gln	Leu	Ile	Arg	Ala	Ile	Asp	Lys	Gln	Gln	Ala	Leu	Lys	
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Ser	Ala	Arg	Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu	
225					230					235					240	
Ile	Gly	Ala	Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met	
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Pro	Ile	Gln	His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn	
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Ser	Ser	Gln	Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val	
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Lys	Glu	Ser	Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu	
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Phe	Asp	Arg	Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His	
			325					330						335		
Ala	Tyr	Ser	Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile	
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Lys	Ala	Leu	Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys	
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	370					375					380					
Glu	Tyr	Phe	Tyr	Lys	Ala	Arg	Asp	Leu	Arg	Trp	Ala	Pro	Glu	Val	Asp	
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Gly	His	Tyr	Thr	Ile	Ala	Pro	Ser	Glu	Phe	Lys	Asp	Asn	Ile	Leu	Leu	
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tgttttcact ttaatttttg cccttttctt tctcatttcg tttaaaaaac ctttaactca 180
agtcttggtg attgtttta atg gtt ttt ttg ttt ttt agg tgt tat ttc caa 232
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              1             5             10

gcg tct ttg aaa gaa act ttc gca att aat cat tta aaa aca atg tct 280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser
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ttt aaa tgg ctc act ctg gct ttt ttg ggc gtg ttt tta agc atc ttc 328
Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe
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cct aac atg ttt aac atg cat gat agc caa act ttc cgc tac aat tta 376
Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu
              45             50             55

ttc gct cta aac atg tcc tta act tat gct tgc ggg gcg tta tgc ttg 424
Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu
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ctt ttt gcc agt tgc tta aga atc aaa ttg aat caa aaa atc ctt ttt 472
Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe
              80             85             90

tac agc atg gct gtt gca aat ttc atc aac ggc ttg ctc tca ttg gtg 520
Tyr Ser Met Ala Val Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val
              95             100             105

caa aaa att tat ttt aac atg ccc aga gcg caa ggg ttt agc acg gtt 568
Gln Lys Ile Tyr Phe Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val
              110             115             120

aag gag tat gtg gtt tta gtg agc gtg tcc att tta ggc tgt tat att 616
Lys Glu Tyr Val Val Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile
              125             130             135

tat gcg ctt tat tcg cac aat caa aaa gaa aaa ctt ttt ttc acg ctt 664
Tyr Ala Leu Tyr Ser His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu
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tct gtt ttt gtg ggg ttt tta gtc gtt att tta agc gcc aca agg agc 712
Ser Val Phe Val Gly Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser
              160             165             170

gcg aca atc gct ttt gtt att act ttt tta atc ctt tct tgc ttt att 760
Ala Thr Ile Ala Phe Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile
              175             180             185

tta tac gcc aaa aaa tcg ctc aaa cca ttg ggt tat atg gtg gtc gtg 808
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Ser	Leu	Ile	Leu	Ser	Ala	Leu	Tyr	Val	Gly	Ser	Asn	Ala	Leu	Glu	Lys		
	205					210					215						
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Lys	Gly	Ala	Ile	Glu	Gln	Ser	Arg	Val	Gln	Asn	Gln	Ser	Phe	Glu	Glu		
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Asp	Leu	Lys	Arg	Tyr	Ala	Lys	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Gly	Trp		
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Arg	Leu	Glu	Arg	Trp	Lys	Glu	Ala	Leu	Thr	Val	Leu	Arg	Leu	Arg	Pro		
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Phe	Phe	Gly	Met	Ala	Ala	Ser	Glu	Lys	Cys	Gln	Arg	Leu	Glu	Glu	Ile		
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Leu	Ser	Leu	Ser	Lys	Ser	Tyr	Arg	Ala	Lys	Asp	Leu	Ile	Leu	Cys	Tyr		
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Glu	Arg	Tyr	Asp	Asn	Gln	Ile	Ile	His	Ile	Leu	Ala	Thr	Arg	Gly	Ile		
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Ile	Gly	Phe	Leu	Ile	Trp	Leu	Phe	Phe	Leu	Leu	Val	Ile	Val	Lys	Ile		
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Phe	Trp	Ser	Gly	Ile	Lys	Gln	Asn	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Leu		
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atg	aca	ctc	gcc	ttt	tac	ctc	att	ttt	ggc	att	ggg	ttt	gac	ccc	ttt	1288	
Met	Thr	Leu	Ala	Phe	Tyr	Leu	Ile	Phe	Gly	Ile	Gly	Phe	Asp	Pro	Phe		
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gat	ttc	ttc	att	acg	gga	agt	ttt	ttt	gta	gga	atg	atc	atg	atg	gct	1336	
Asp	Phe	Phe	Ile	Thr	Gly	Ser	Phe	Phe	Val	Gly	Met	Ile	Met	Met	Ala		
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ggt	ttt	tta	aaa	aaa	gat	aaa	agt	gct	ttt	tagcatcaag	gggtttgaca					1386	
Val	Phe	Leu	Lys	Lys	Asp	Lys	Ser	Ala	Phe								
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<212> PRT

<213> Helicobacter pylori

<400> 68

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Met	His	Asp	Ser	Gln	Thr	Phe	Arg	Tyr	Asn	Leu	Phe	Ala	Leu	Asn	Met
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Leu	Arg	Ile	Lys	Leu	Asn	Gln	Lys	Ile	Leu	Phe	Tyr	Ser	Met	Ala	Val
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Ala	Asn	Phe	Ile	Asn	Gly	Leu	Leu	Ser	Leu	Val	Gln	Lys	Ile	Tyr	Phe
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Asn	Met	Pro	Arg	Ala	Gln	Gly	Phe	Ser	Thr	Val	Lys	Glu	Tyr	Val	Val
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Leu	Val	Ser	Val	Ser	Ile	Leu	Gly	Cys	Tyr	Ile	Tyr	Ala	Leu	Tyr	Ser
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Phe	Leu	Val	Val	Ile	Leu	Ser	Ala	Thr	Arg	Ser	Ala	Thr	Ile	Ala	Phe
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Val	Ile	Thr	Phe	Leu	Ile	Leu	Ser	Cys	Phe	Ile	Leu	Tyr	Ala	Lys	Lys
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Ser	Leu	Lys	Pro	Leu	Gly	Tyr	Met	Val	Val	Val	Ser	Leu	Ile	Leu	Ser
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Gln	Ser	Arg	Val	Gln	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Leu	Lys	Arg	Tyr
225					230					235					240
Ala	Lys	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Gly	Trp	Arg	Leu	Glu	Arg	Trp
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Lys	Glu	Ala	Leu	Thr	Val	Leu	Arg	Leu	Arg	Pro	Phe	Phe	Gly	Met	Ala
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Ala	Ser	Glu	Lys	Cys	Gln	Arg	Leu	Glu	Glu	Ile	Leu	Ser	Leu	Ser	Lys
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	290					295					300				
Gln	Ile	Ile	His	Ile	Leu	Ala	Thr	Arg	Gly	Ile	Ile	Gly	Phe	Leu	Ile
305					310					315					320
Trp	Leu	Phe	Phe	Leu	Leu	Val	Ile	Val	Lys	Ile	Phe	Trp	Ser	Gly	Ile
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Lys	Gln	Asn	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Leu	Met	Thr	Leu	Ala	Phe
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Tyr	Leu	Ile	Phe	Gly	Ile	Gly	Phe	Asp	Pro	Phe	Asp	Phe	Phe	Ile	Thr
		355					360					365			
Gly	Ser	Phe	Phe	Val	Gly	Met	Ile	Met	Met	Ala	Val	Phe	Leu	Lys	Lys
	370					375					380				
Asp	Lys	Ser	Ala	Phe											
385															

<210> 69
 <211> 1252
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (89)...(1198)

<400> 69
 aaaaaggaaa tagcacgatg aaacctaaag gggatattag cgtaaataatg ctaatatagt 60
 agaacattat gactacaaaa agggatgat atg ctg atc tcc ata gcg ttt tta 112
 Met Leu Ile Ser Ile Ala Phe Leu
 1 5

ttg gtt tta tat ctt ttg aat tat agt tct ttc agg atg ttg aaa tcg 160
 Leu Val Leu Tyr Leu Leu Asn Tyr Ser Ser Phe Arg Met Leu Lys Ser
 10 15 20

ttt tta acc tta aag aaa atc tct caa tac gct tat tta tgg ttt ttt 208
 Phe Leu Thr Leu Lys Lys Ile Ser Gln Tyr Ala Tyr Leu Trp Phe Phe
 25 30 35 40

atc ctt ttg agc ata ggc gag gcg gct ttt gtt ttt tat aga aat att 256
 Ile Leu Leu Ser Ile Gly Glu Ala Ala Phe Val Phe Tyr Arg Asn Ile
 45 50 55

atg cct agc cat ttg ttt gtt ttg act tca gcg tgt tcg ttt gtg tct 304
 Met Pro Ser His Leu Phe Val Leu Thr Ser Ala Cys Ser Phe Val Ser
 60 65 70

ttt att att ttt atc ctt tct tta agt ttt tac ggg ttt tcc tat tcc 352
 Phe Ile Ile Phe Ile Leu Ser Leu Ser Phe Tyr Gly Phe Ser Tyr Ser
 75 80 85

ata gaa aaa ata gat ttt ttg cat tca agg cgt aaa agt tta aaa aac 400
 Ile Glu Lys Ile Asp Phe Leu His Ser Arg Arg Lys Ser Leu Lys Asn
 90 95 100

ttt tta aaa ttg ggg ttt tat ctg gcg tta tta ggg tat ttt tgg cgt 448
 Phe Leu Lys Leu Gly Phe Tyr Leu Ala Leu Leu Gly Tyr Phe Trp Arg
 105 110 115 120

ggg ttt tat gaa ggg ttg gcc cgc cct aaa atc aaa gaa acc cct att 496
 Gly Phe Tyr Glu Gly Leu Ala Arg Pro Lys Ile Lys Glu Thr Pro Ile
 125 130 135

tat ttg gat aag ctg gat aaa gaa tta aag att att tta ctc aca gac 544
 Tyr Leu Asp Lys Leu Asp Lys Glu Leu Lys Ile Ile Leu Leu Thr Asp
 140 145 150

atg cat gtg ggg agt ttg ttg caa aaa gat ttt gtt gat tac att gta 592
 Met His Val Gly Ser Leu Leu Gln Lys Asp Phe Val Asp Tyr Ile Val
 155 160 165

gaa gaa gtc aat caa aaa gaa gtg gat atg gtg ctg att ggg ggg gat	640
Glu Glu Val Asn Gln Lys Glu Val Asp Met Val Leu Ile Gly Gly Asp	
170 175 180	
tta gtg gat gaa agc att gaa aaa gtc aaa tct ttt tta ctg cct tta	688
Leu Val Asp Glu Ser Ile Glu Lys Val Lys Ser Phe Leu Leu Pro Leu	
185 190 195 200	
aac aac ctt aaa agc acg cat ggc act ttt tat gtg cca gga aat cat	736
Asn Asn Leu Lys Ser Thr His Gly Thr Phe Tyr Val Pro Gly Asn His	
205 210 215	
gag tat tat cat ggc ata gag ccg att tta tcg ttt ctt gac acg ctt	784
Glu Tyr Tyr His Gly Ile Glu Pro Ile Leu Ser Phe Leu Asp Thr Leu	
220 225 230	
aat ttg acg att tta ggg aat gag tgc gtg cat tta ggg ggg atc aat	832
Asn Leu Thr Ile Leu Gly Asn Glu Cys Val His Leu Gly Gly Ile Asn	
235 240 245	
ttg tgc ggc gtg tat gat tat ttc gca agg aag cgt caa aat ttt gcc	880
Leu Cys Gly Val Tyr Asp Tyr Phe Ala Arg Lys Arg Gln Asn Phe Ala	
250 255 260	
cct gat att gac aaa gct tta aaa aag cgc aat gag agt aag ccc acg	928
Pro Asp Ile Asp Lys Ala Leu Lys Lys Arg Asn Glu Ser Lys Pro Thr	
265 270 275 280	
atc ctt ttg gcc cac caa cct aaa caa att aga agc ctc aaa gaa agc	976
Ile Leu Leu Ala His Gln Pro Lys Gln Ile Arg Ser Leu Lys Glu Ser	
285 290 295	
cac tct gta gat tta gtc ctt tca ggg cat acc cat gca ggg caa atc	1024
His Ser Val Asp Leu Val Leu Ser Gly His Thr His Ala Gly Gln Ile	
300 305 310	
ttt ccc ttt agc ctt tta gtc aag ttg gcg caa acc tat tta cat ggt	1072
Phe Pro Phe Ser Leu Leu Val Lys Leu Ala Gln Thr Tyr Leu His Gly	
315 320 325	
tta tac aag cac agc ccc acc act caa att tat gtg agc agt ggg gca	1120
Leu Tyr Lys His Ser Pro Thr Thr Gln Ile Tyr Val Ser Ser Gly Ala	
330 335 340	
ggg tat tgg ggg att cct tta agg ttt tta gcc cct agc gag atc gca	1168
Gly Tyr Trp Gly Ile Pro Leu Arg Phe Leu Ala Pro Ser Glu Ile Ala	
345 350 355 360	
tac ctt agg ctt tta cct aaa aat caa gct tagttaaaca aaatcttaaa	1218
Tyr Leu Arg Leu Leu Pro Lys Asn Gln Ala	
365 370	
atcttaatcg taatcaagcg gttaaaaaata agaa	1252

<210> 70

<211> 370
 <212> PRT
 <213> Helicobacter pylori

<400> 70
 Met Leu Ile Ser Ile Ala Phe Leu Leu Val Leu Tyr Leu Leu Asn Tyr
 1 5 10 15
 Ser Ser Phe Arg Met Leu Lys Ser Phe Leu Thr Leu Lys Lys Ile Ser
 20 25 30
 Gln Tyr Ala Tyr Leu Trp Phe Phe Ile Leu Leu Ser Ile Gly Glu Ala
 35 40 45
 Ala Phe Val Phe Tyr Arg Asn Ile Met Pro Ser His Leu Phe Val Leu
 50 55 60
 Thr Ser Ala Cys Ser Phe Val Ser Phe Ile Ile Phe Ile Leu Ser Leu
 65 70 75 80
 Ser Phe Tyr Gly Phe Ser Tyr Ser Ile Glu Lys Ile Asp Phe Leu His
 85 90 95
 Ser Arg Arg Lys Ser Leu Lys Asn Phe Leu Lys Leu Gly Phe Tyr Leu
 100 105 110
 Ala Leu Leu Gly Tyr Phe Trp Arg Gly Phe Tyr Glu Gly Leu Ala Arg
 115 120 125
 Pro Lys Ile Lys Glu Thr Pro Ile Tyr Leu Asp Lys Leu Asp Lys Glu
 130 135 140
 Leu Lys Ile Ile Leu Leu Thr Asp Met His Val Gly Ser Leu Leu Gln
 145 150 155 160
 Lys Asp Phe Val Asp Tyr Ile Val Glu Glu Val Asn Gln Lys Glu Val
 165 170 175
 Asp Met Val Leu Ile Gly Gly Asp Leu Val Asp Glu Ser Ile Glu Lys
 180 185 190
 Val Lys Ser Phe Leu Leu Pro Leu Asn Asn Leu Lys Ser Thr His Gly
 195 200 205
 Thr Phe Tyr Val Pro Gly Asn His Glu Tyr Tyr His Gly Ile Glu Pro
 210 215 220
 Ile Leu Ser Phe Leu Asp Thr Leu Asn Leu Thr Ile Leu Gly Asn Glu
 225 230 235 240
 Cys Val His Leu Gly Gly Ile Asn Leu Cys Gly Val Tyr Asp Tyr Phe
 245 250 255
 Ala Arg Lys Arg Gln Asn Phe Ala Pro Asp Ile Asp Lys Ala Leu Lys
 260 265 270
 Lys Arg Asn Glu Ser Lys Pro Thr Ile Leu Leu Ala His Gln Pro Lys
 275 280 285
 Gln Ile Arg Ser Leu Lys Glu Ser His Ser Val Asp Leu Val Leu Ser
 290 295 300
 Gly His Thr His Ala Gly Gln Ile Phe Pro Phe Ser Leu Leu Val Lys
 305 310 315 320
 Leu Ala Gln Thr Tyr Leu His Gly Leu Tyr Lys His Ser Pro Thr Thr
 325 330 335
 Gln Ile Tyr Val Ser Ser Gly Ala Gly Tyr Trp Gly Ile Pro Leu Arg
 340 345 350
 Phe Leu Ala Pro Ser Glu Ile Ala Tyr Leu Arg Leu Leu Pro Lys Asn
 355 360 365
 Gln Ala
 370

<210> 71
 <211> 431
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (103)...(381)

<400> 71
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 gcttgcttta gcgagtttgt ggggtgaaacg tacgccttgc tc atg att ttt gtc 114
 Met Ile Phe Val
 1

aat aaa tat ctc tat ggg att aaa agc gtt gtg cct ttg gcg gtt ggt 162
 Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Val Gly
 5 10 15 20

ttt agc aaa tac cct tta aaa aag ttt tta tgg ctt aat gtt ttt tcc 210
 Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
 25 30 35

agt ttt ttg tgg gcg ctc atc gtg ggg agc gtt tct ttt caa gcg agc 258
 Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
 40 45 50

gat tgg gtg aaa acg ctg tat gaa agg ctt tct cat tac act tcg ttt 306
 Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
 55 60 65

ttt atc ata agt ttt gtt ctt ata gcg ctt tta ata tgg ttt tta ttg 354
 Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
 70 75 80

aaa cga tat tcg cgc aaa atg ggt ttt taagcaagat gtttaattaa 401
 Lys Arg Tyr Ser Arg Lys Met Gly Phe
 85 90

atgcgctaga ctacgccac aagcattcgc 431

<210> 72
 <211> 93
 <212> PRT
 <213> Helicobacter pylori

<400> 72
 Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro
 1 5 10 15
 Leu Ala Val Gly Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu
 20 25 30
 Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser
 35 40 45
 Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His
 50 55 60

Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile
65 70 75 80
Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe
85 90

<210> 73
<211> 1281
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (70)...(1227)

<400> 73
tagcatcaat accccttaaa taaaagatat aatgctgtat tataagctag ttttaattac 60
aattttcaa atg tta agg aaa aac att tta gct tac tat ggg gcg aat ttt 111
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe
1 5 10

ctc tta atc atc gct caa agc tta ccc cat gcg att tta acc ccc ttg 159
Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu
15 20 25 30

ttg ctt tct aaa ggg ctt agt ttg agt gaa atc ttg ctc gtg caa acc 207
Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr
35 40 45

ttt ttt agc ttt tgc gtg cta gtg gct gaa tac cca agc ggc gtt tta 255
Phe Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu
50 55 60

gcg gat ttg atg agc cga aaa aat tta ttc ctg gtt tct aat gcc ttt 303
Ala Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe
65 70 75

tta atc gct agt ttt tcg ttt gtg ctg ttt ttt gat agc ttt att ttc 351
Leu Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe
80 85 90

atg ctt tta gcg tgg ggg ttg tat ggt ttg tat agc gca tgc tct agc 399
Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser
95 100 105 110

ggc acg att gaa gct tca ctc atc aca gac att aag gaa aac aaa aaa 447
Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys
115 120 125

gat tta tcc aag ttt tta gcc aaa aac aat caa att act tat tta ggc 495
Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly
130 135 140

atg att ata ggg agt tct ttg gga tcg ttt ttg tat ctc aaa gtc cat 543
Met Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His

145	150	155	
gcg atg ctg tat att gtg ggg att ttt tta atc atg ctc tgt gtg cta			591
Ala Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu			
160	165	170	
acg atc att ttt tat ttt aaa gag aaa gaa ggg gat ttt aaa agc caa			639
Thr Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln			
175	180	185	190
aaa agc ctg aaa ctc ctt aaa gag caa gtc aaa ggc agt ctt aaa gag			687
Lys Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu			
	195	200	205
ctt aaa gat aac ccc aaa ctt aaa att ctg tta gtg ggg cat ttg att			735
Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile			
	210	215	220
acg ccc gtc ttt ttt atg agc cat ttt caa atg tgg caa gcg tat ttt			783
Thr Pro Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe			
	225	230	235
tta aaa caa ggc gtt aaa gag caa tac ctt ttt gtg ttt tat atc gct			831
Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala			
	240	245	250
ttt caa gtg att tct att ctc att cat ttt tta aaa gcc tct agt tat			879
Phe Gln Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr			
255	260	265	270
agc caa aaa atc gcc ttg agt tcg ctt gtg gtg ttg tta ggc gtt agc			927
Ser Gln Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser			
	275	280	285
ccc tta ttg ctt agc aat atc cct tat tgt ttc ata ggg gtg tat gcg			975
Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala			
	290	295	300
ctc atg gtg gcg ttt ttc act tac atg agc tat tgc tta aac tat caa			1023
Leu Met Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln			
	305	310	315
ttc tcc aaa ttc gtt tct aaa aac aac att tcc tcg ctc tca tcg ctt			1071
Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu			
	320	325	330
tta tca agc tgt gtg cgc gtg gtc tct gtg cta atc tta tcg ctc agc			1119
Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser			
335	340	345	350
agt ctg gaa ctg cgt tac ttc tca ccc cta act atc ata acc atg cat			1167
Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His			
	355	360	365
ttt gcc ttg acg ctt atc atc ctc ttt ttc ttt ttg tat aag gct aag			1215

Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys
 370 375 380

ccg ttt gat gag tgagcggctt taagagtgca accttttagc gatttctata 1267
 Pro Phe Asp Glu
 385

gcaacatcat agcc 1281

<210> 74
 <211> 386
 <212> PRT
 <213> Helicobacter pylori

<400> 74
 Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
 1 5 10 15
 Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
 20 25 30
 Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
 35 40 45
 Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
 50 55 60
 Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile
 65 70 75 80
 Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu
 85 90 95
 Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
 100 105 110
 Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
 115 120 125
 Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
 130 135 140
 Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
 145 150 155 160
 Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile
 165 170 175
 Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser
 180 185 190
 Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
 195 200 205
 Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
 210 215 220
 Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
 225 230 235 240
 Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
 245 250 255
 Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln
 260 265 270
 Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro Leu
 275 280 285
 Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met
 290 295 300
 Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser
 305 310 315 320

ccc tct atc tta tgg att ttg ata ggc tgc gtt tta ggg ggt tgc gtg	496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val	
125 130 135 140	
cat gat ttt gtg gtg ctt ttt gct tct att agg cgc gat ggc aag tct	544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser	
145 150 155	
tta ggc gaa atg atc aaa ctt gaa atg ggc caa ttt gta ggc atg atc	592
Leu Gly Glu Met Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile	
160 165 170	
gca agt ctg ggc att tta ggg atc atg ctc att atc att gcg att tta	640
Ala Ser Leu Gly Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu	
175 180 185	
gcg atg gtg gtg gtg aag gct tta gcg cat tgc cct tgg ggc ttt ttt	688
Ala Met Val Val Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe	
190 195 200	
acg atc gca atg act att ccc att gcg att ctt atg ggg ctt tac atg	736
Thr Ile Ala Met Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met	
205 210 215 220	
cgg ttt ttc agg cca cac aag att tta gag gtt tct gtt att ggc ttt	784
Arg Phe Phe Arg Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe	
225 230 235	
atc cta ttg att ata gcg att tat gcg ggt aaa tac gtt tct tta gat	832
Ile Leu Leu Ile Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp	
240 245 250	
cct aaa tta gcg tca ata ttc act ttt gag gcc agt tct tta gcg tgg	880
Pro Lys Leu Ala Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp	
255 260 265	
atg atc atg ggc tat ggg ttt gtg gct tct att tta ccg gta tgg ttt	928
Met Ile Met Gly Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe	
270 275 280	
tta ctc gct cca cga gat tat cta agc act ttt tta aaa att ggc gtt	976
Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val	
285 290 295 300	
ata ggg gtg ttg gtt gtg gcc att att ttt gtc gct ccg cct tta caa	1024
Ile Gly Val Leu Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln	
305 310 315	
atc cct aaa atc acg ccc ttt gta gat ggc agt ggg cct gtg ttt gca	1072
Ile Pro Lys Ile Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala	
320 325 330	
gga agc gtg ttc cct ttc ttg ttt atc acg gtg gct tgc ggg acg att	1120
Gly Ser Val Phe Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile	
335 340 345	

agc gga ttc cat gct tta att tct tca ggc acg acc cct aaa atg ctc	1168
Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu	
350 355 360	
gct aaa gaa agc gac gca agg cta gtg ggc tat ggc tct atg gtg atg	1216
Ala Lys Glu Ser Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met	
365 370 375 380	
gag agc gtt gtg gct ctt atg gcg ttg gtg tgc gca ggg atc ttg cac	1264
Glu Ser Val Val Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His	
385 390 395	
cca ggg ctt tat ttc gct atc aat tgc cca gaa gtg agc atc ggt aaa	1312
Pro Gly Leu Tyr Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys	
400 405 410	
gat ata gct gat gcg gct tca gtg att agc tca tgg ggg ttt aat atc	1360
Asp Ile Ala Asp Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile	
415 420 425	
agc gct gaa gaa att cgt gag atg act aaa aac atc ggc gaa agc tcc	1408
Ser Ala Glu Glu Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser	
430 435 440	
att ttg agc cgc acc ggt ggg gcg ccc act ttt gcg atc ggt tta gcg	1456
Ile Leu Ser Arg Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala	
445 450 455 460	
atg att gtg tat cac att tta ggg gat cca agc gtg atg gcg ttt tgg	1504
Met Ile Val Tyr His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp	
465 470 475	
tat cat ttt gcg att ttg ttt gaa gct ttg ttc att tta acc gct gtg	1552
Tyr His Phe Ala Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val	
480 485 490	
gat gct ggc aca cga acc gct cgt ttc atg att caa gat ttg ctc ggt	1600
Asp Ala Gly Thr Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly	
495 500 505	
aat gtt tat aag cct ttg ggc gat ctt agc tct tat aag gct ggg att	1648
Asn Val Tyr Lys Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile	
510 515 520	
ttt gcc act ctt ttg tgc gtg gca ggg tgg ggg tat ttc ttg tat caa	1696
Phe Ala Thr Leu Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln	
525 530 535 540	
ggc acg att gat cct aaa ggg ggg att tat acg cta tgg cct tta ttt	1744
Gly Thr Ile Asp Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe	
545 550 555	
ggc gtg agc aat cag atg tta gcg ggc atg gcg ttg ttg ttg gtc acg	1792
Gly Val Ser Asn Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr	

560	565	570	
gtg gtg ttg ttt aaa atg ggg cgt ttt aag ggg gcg atg ata agc gcc			1840
Val Val Leu Phe Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala			
575	580	585	
tta ccg gca gtt ttg att tta tcc atc act ttt tat agc ggt att tta			1888
Leu Pro Ala Val Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu			
590	595	600	
aag gtg gtg cca aag agc gat aac agc gtg ctg aat aat gtt tcc cat			1936
Lys Val Val Pro Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His			
605	610	615	620
gtg gcg caa atg caa atc atc aaa gaa aaa atg gct acc act acc gat			1984
Val Ala Gln Met Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp			
	625	630	635
gaa aaa gcg ctc aaa acg ctc caa aaa tcc ttt ttt aac cac gct att			2032
Glu Lys Ala Leu Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile			
	640	645	650
gat gcg att ttg tgc gtg ttt ttc atg ctt gtg gcg cta ttg gtt tta			2080
Asp Ala Ile Leu Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu			
	655	660	665
atc gtg agc gtt agg att tgc tca aac gct tat ttt aaa aac aaa att			2128
Ile Val Ser Val Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile			
	670	675	680
tac cca ccg ctg gct gaa acg ccc tac atc aaa gcc tct tgaataaaaa			2177
Tyr Pro Pro Leu Ala Glu Thr Pro Tyr Ile Lys Ala Ser			
685	690	695	
aggggtttta acccccttta aatccataga aaaaagtttg a			2218
<210> 76			
<211> 697			
<212> PRT			
<213> Helicobacter pylori			
<400> 76			
Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln Lys Ser Leu Val			
1 5 10 15			
Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala Ile Cys Leu Gly			
20 25 30			
Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr Leu Trp Leu Val			
35 40 45			
Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg Phe Tyr Ser His			
50 55 60			
Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser Arg Ala Thr Pro			
65 70 75 80			
Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro Thr Asp Lys Ala			
85 90 95			
Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu			

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Val	Gly	Pro	Ile	Leu	Ala	Ala	Gln	Met	Gly	Tyr	Leu	Pro	Ser	Ile	Leu		
		115					120					125					
Trp	Ile	Leu	Ile	Gly	Ser	Val	Leu	Gly	Gly	Cys	Val	His	Asp	Phe	Val		
		130					135					140					
Val	Leu	Phe	Ala	Ser	Ile	Arg	Arg	Asp	Gly	Lys	Ser	Leu	Gly	Glu	Met		
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			165						170					175			
Ile	Leu	Gly	Ile	Met	Leu	Ile	Ile	Ile	Ala	Ile	Leu	Ala	Met	Val	Val		
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Val	Lys	Ala	Leu	Ala	His	Ser	Pro	Trp	Gly	Phe	Phe	Thr	Ile	Ala	Met		
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Thr	Ile	Pro	Ile	Ala	Ile	Leu	Met	Gly	Leu	Tyr	Met	Arg	Phe	Phe	Arg		
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Pro	His	Lys	Ile	Leu	Glu	Val	Ser	Val	Ile	Gly	Phe	Ile	Leu	Leu	Ile		
225					230					235					240		
Ile	Ala	Ile	Tyr	Ala	Gly	Lys	Tyr	Val	Ser	Leu	Asp	Pro	Lys	Leu	Ala		
			245						250					255			
Ser	Ile	Phe	Thr	Phe	Glu	Ala	Ser	Ser	Leu	Ala	Trp	Met	Ile	Met	Gly		
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Tyr	Gly	Phe	Val	Ala	Ser	Ile	Leu	Pro	Val	Trp	Phe	Leu	Leu	Ala	Pro		
		275					280					285					
Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Leu	Lys	Ile	Gly	Val	Ile	Gly	Val	Leu		
		290				295					300						
Val	Val	Ala	Ile	Ile	Phe	Val	Ala	Pro	Pro	Leu	Gln	Ile	Pro	Lys	Ile		
305					310					315					320		
Thr	Pro	Phe	Val	Asp	Gly	Ser	Gly	Pro	Val	Phe	Ala	Gly	Ser	Val	Phe		
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Pro	Phe	Leu	Phe	Ile	Thr	Val	Ala	Cys	Gly	Thr	Ile	Ser	Gly	Phe	His		
			340					345					350				
Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	Lys	Met	Leu	Ala	Lys	Glu	Ser		
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Asp	Ala	Arg	Leu	Val	Gly	Tyr	Gly	Ser	Met	Val	Met	Glu	Ser	Val	Val		
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Phe	Ala	Ile	Asn	Ser	Pro	Glu	Val	Ser	Ile	Gly	Lys	Asp	Ile	Ala	Asp		
			405						410					415			
Ala	Ala	Ser	Val	Ile	Ser	Ser	Trp	Gly	Phe	Asn	Ile	Ser	Ala	Glu	Glu		
			420					425					430				
Ile	Arg	Glu	Met	Thr	Lys	Asn	Ile	Gly	Glu	Ser	Ser	Ile	Leu	Ser	Arg		
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Thr	Gly	Gly	Ala	Pro	Thr	Phe	Ala	Ile	Gly	Leu	Ala	Met	Ile	Val	Tyr		
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His	Ile	Leu	Gly	Asp	Pro	Ser	Val	Met	Ala	Phe	Trp	Tyr	His	Phe	Ala		
465					470					475					480		
Ile	Leu	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Ala	Val	Asp	Ala	Gly	Thr		
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Arg	Thr	Ala	Arg	Phe	Met	Ile	Gln	Asp	Leu	Leu	Gly	Asn	Val	Tyr	Lys		
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Pro	Leu	Gly	Asp	Leu	Ser	Ser	Tyr	Lys	Ala	Gly	Ile	Phe	Ala	Thr	Leu		
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Leu	Cys	Val	Ala	Gly	Trp	Gly	Tyr	Phe	Leu	Tyr	Gln	Gly	Thr	Ile	Asp		
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Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe Gly Val Ser Asn
 545 550 555 560
 Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr Val Val Leu Phe
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 Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala Leu Pro Ala Val
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 Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu Lys Val Val Pro
 595 600 605
 Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His Val Ala Gln Met
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 Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp Glu Lys Ala Leu
 625 630 635 640
 Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile Asp Ala Ile Leu
 645 650 655
 Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu Ile Val Ser Val
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 Ala Glu Thr Pro Tyr Ile Lys Ala Ser
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 atg caa aaa act tct aac act ctg gcg ctg ggg agt ttg aca gcg cta 168
 Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu
 1 5 10 15
 ttc ttt cta atg ggt ttt atc acg gtt tta aac gat att tta atc cca 216
 Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro
 20 25 30
 cac tta aag ccc att ttt gac ttg acc tat ttt gaa gct tca ctc att 264
 His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile
 35 40 45
 caa ttt tgc ttt ttt ggg gcg tat ttc atc atg gga gga gtt ttt ggg 312
 Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly
 50 55 60
 aat gtg atc agt aaa atc ggc tac cct ttt ggc gtg gtg ctt ggt ttt 360

Asn	Val	Ile	Ser	Lys	Ile	Gly	Tyr	Pro	Phe	Gly	Val	Val	Leu	Gly	Phe									
65					70					75					80									
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Val	Ile	Thr	Ala	Thr	Gly	Cys	Ala	Leu	Phe	Tyr	Pro	Ala	Ala	His	Phe									
				85					90					95										
gga	tcc	tat	ggg	ttt	ttt	tta	gga	gcg	ttg	ttt	att	tta	gcg	agc	ggg	456								
Gly	Ser	Tyr	Gly	Phe	Phe	Leu	Gly	Ala	Leu	Phe	Ile	Leu	Ala	Ser	Gly									
			100					105					110											
att	gtg	tgc	ttg	caa	acc	gct	ggt	aat	ccc	ttt	gta	acc	ttg	ctt	tct	504								
Ile	Val	Cys	Leu	Gln	Thr	Ala	Gly	Asn	Pro	Phe	Val	Thr	Leu	Leu	Ser									
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aaa	ggt	aaa	gaa	gcc	aga	aat	ttg	ggt	tta	gtc	cag	gcg	ttc	aat	tcg	552								
Lys	Gly	Lys	Glu	Ala	Arg	Asn	Leu	Val	Leu	Val	Gln	Ala	Phe	Asn	Ser									
	130					135					140													
ctt	ggc	aca	act	tta	ggg	cct	att	ttt	ggg	agc	ttg	ttg	att	ttt	agc	600								
Leu	Gly	Thr	Thr	Leu	Gly	Pro	Ile	Phe	Gly	Ser	Leu	Leu	Ile	Phe	Ser									
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Thr	Thr	Lys	Met	Gly	Asp	Asn	Ala	Ser	Leu	Ile	Asp	Lys	Leu	Ala	Asp									
				165					170					175										
gct	aaa	agc	gtt	caa	atg	cct	tat	ttg	ggc	ttg	gcg	gtg	ttt	tcg	ctt	696								
Ala	Lys	Ser	Val	Gln	Met	Pro	Tyr	Leu	Gly	Leu	Ala	Val	Phe	Ser	Leu									
			180					185					190											
ctt	tta	gcg	ctc	atc	atg	tat	ctt	ttg	aaa	ttg	cct	gat	gtg	gaa	aaa	744								
Leu	Leu	Ala	Leu	Ile	Met	Tyr	Leu	Leu	Lys	Leu	Pro	Asp	Val	Glu	Lys									
		195					200					205												
gaa	atg	ccc	aaa	gag	acg	act	caa	aaa	agc	ttg	ttt	tcg	cac	aaa	cac	792								
Glu	Met	Pro	Lys	Glu	Thr	Thr	Gln	Lys	Ser	Leu	Phe	Ser	His	Lys	His									
	210					215					220													
ttt	ggt	ttt	ggg	gct	tgg	gga	tct	ttt	ttt	atg	tgg	ggg	gag	aan	tgg	840								
Phe	Val	Phe	Gly	Ala	Trp	Gly	Ser	Phe	Phe	Met	Trp	Gly	Glu	Xaa	Trp									
225					230					235					240									
cga	ttg	gct	cat	tct	tgg	tgc	taagcttttga aaagcttttg aatttagact									891								
Arg	Leu	Ala	His	Ser	Trp	Cys																		
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ctcaatcaag cgcgcatc																911								
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 His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile
 35 40 45
 Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly
 50 55 60
 Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe
 65 70 75 80
 Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe
 85 90 95
 Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly
 100 105 110
 Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser
 115 120 125
 Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser
 130 135 140
 Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser
 145 150 155 160
 Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp
 165 170 175
 Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu
 180 185 190
 Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys
 195 200 205
 Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His
 210 215 220
 Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp
 225 230 235 240
 Arg Leu Ala His Ser Trp Cys
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 Met Ser Lys
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 Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr Lys Thr Pro

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aca gat tta gaa gtc cct aat tta tta tta tta caa cga gac agc tat			153
Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg Asp Ser Tyr			
20	25	30	35
gat tct ttc ttg tat tct aaa gag ggt aaa gag agc ggg att gaa aag			201
Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly Ile Glu Lys			
	40	45	50
gtt ttt aaa tcc att ttc cct atc caa gat gag cat aac cgc atc act			249
Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn Arg Ile Thr			
	55	60	65
tta gaa tac gcg ggt tgc gaa ttt ggc aag tct aaa tac acc gtt aga			297
Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr Thr Val Arg			
	70	75	80
gaa gcg atg gag agg ggc att acc tac tct atc cct ctc aaa att aag			345
Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu Lys Ile Lys			
	85	90	95
gtg cgc ttg atc ttg tgg gaa aaa gat acc aag agt ggc gaa aag aac			393
Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly Glu Lys Asn			
100	105	110	115
ggc att aag gat att aaa gaa caa agc att ttc att cgt gag atc cct			441
Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg Glu Ile Pro			
	120	125	130
ttg atg aca gaa cgc act tca ttt att att aat ggg gtg gag cgc gtg			489
Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val Glu Arg Val			
	135	140	145
gtg gtc aat caa ctc cac aga agc ccc ggt gtg att ttc aaa gaa gaa			537
Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe Lys Glu Glu			
	150	155	160
gag tct agc act tct tta aac aag ctc att tac aca ggg caa atc att			585
Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile			
	165	170	175
cct gat agg ggt tgc tgg ttg tat ttt gaa tac gat tct aaa gat gtt			633
Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val			
180	185	190	195
tta tac gct cgt atc aat aaa cgc cgt aaa gtg cct gtt acc att tta			681
Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu			
	200	205	210
ttc agg gcg atg gat tat caa aaa caa gac atc atc aaa atg ttc tac			729
Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr			
	215	220	225
ccg ctt gtt aaa gtg cgt tat gaa aac gat aaa tat ttg atc ccg ttt			777

Pro	Leu	Val	Lys	Val	Arg	Tyr	Glu	Asn	Asp	Lys	Tyr	Leu	Ile	Pro	Phe		
		230					235					240					
gct	tca	tta	gac	gcc	aat	caa	aga	atg	gaa	ttt	gac	ttg	aaa	gat	cct	825	
Ala	Ser	Leu	Asp	Ala	Asn	Gln	Arg	Met	Glu	Phe	Asp	Leu	Lys	Asp	Pro		
		245				250					255						
caa	ggc	aag	gtt	att	ctt	tta	gcg	ggt	aaa	aag	ctc	act	tca	aga	aag	873	
Gln	Gly	Lys	Val	Ile	Leu	Leu	Ala	Gly	Lys	Lys	Leu	Thr	Ser	Arg	Lys		
		260			265					270					275		
att	aaa	gag	ctt	aaa	gaa	aac	cat	tta	gaa	tgg	gtg	gaa	tac	cct	atg	921	
Ile	Lys	Glu	Leu	Lys	Glu	Asn	His	Leu	Glu	Trp	Val	Glu	Tyr	Pro	Met		
				280					285					290			
gat	att	tta	ctc	aat	cgc	cat	tta	gct	gag	cct	gtt	atg	gta	ggg	aaa	969	
Asp	Ile	Leu	Leu	Asn	Arg	His	Leu	Ala	Glu	Pro	Val	Met	Val	Gly	Lys		
				295				300					305				
gaa	gtc	tta	ttg	gac	atg	ctc	act	cag	cta	gat	aaa	aac	aaa	tta	gaa	1017	
Glu	Val	Leu	Leu	Asp	Met	Leu	Thr	Gln	Leu	Asp	Lys	Asn	Lys	Leu	Glu		
		310					315					320					
aaa	atc	cac	gat	tta	ggc	gtg	caa	gaa	ttt	gtg	atc	atc	aac	gat	ctg	1065	
Lys	Ile	His	Asp	Leu	Gly	Val	Gln	Glu	Phe	Val	Ile	Ile	Asn	Asp	Leu		
		325				330					335						
gcg	tta	ggg	cat	gac	gct	tcc	att	atc	caa	tct	ttt	tca	gcc	gat	tct	1113	
Ala	Leu	Gly	His	Asp	Ala	Ser	Ile	Ile	Gln	Ser	Phe	Ser	Ala	Asp	Ser		
		340			345				350					355			
gag	tct	ttg	aaa	tta	ctc	aag	caa	acc	gaa	aaa	att	gat	gat	gaa	aac	1161	
Glu	Ser	Leu	Lys	Leu	Leu	Lys	Gln	Thr	Glu	Lys	Ile	Asp	Asp	Glu	Asn		
				360					365					370			
gct	cta	gcg	gcg	att	cgt	atc	cat	aag	gtt	atg	aaa	cca	ggc	gat	ccc	1209	
Ala	Leu	Ala	Ala	Ile	Arg	Ile	His	Lys	Val	Met	Lys	Pro	Gly	Asp	Pro		
				375				380					385				
gtt	acg	act	gaa	gtg	gct	aag	cag	ttt	gtc	aaa	aaa	ctt	ttc	ttt	gat	1257	
Val	Thr	Thr	Glu	Val	Ala	Lys	Gln	Phe	Val	Lys	Lys	Leu	Phe	Phe	Asp		
		390					395					400					
cca	gaa	cgc	tat	gat	ttg	acc	atg	gtg	ggc	cgc	atg	aaa	atg	aat	cac	1305	
Pro	Glu	Arg	Tyr	Asp	Leu	Thr	Met	Val	Gly	Arg	Met	Lys	Met	Asn	His		
		405				410					415						
aag	tta	ggc	ttg	cat	gtg	cct	gat	tac	att	acg	act	tta	acg	cat	gaa	1353	
Lys	Leu	Gly	Leu	His	Val	Pro	Asp	Tyr	Ile	Thr	Thr	Leu	Thr	His	Glu		
		420			425					430					435		
gat	att	atc	acc	acc	gtt	aaa	tac	ctc	atg	aag	atc	aaa	aac	aat	caa	1401	
Asp	Ile	Ile	Thr	Thr	Val	Lys	Tyr	Leu	Met	Lys	Ile	Lys	Asn	Asn	Gln		
				440					445					450			

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Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala	
455 460 465	
gta ggg gaa ttg ttg gcc aat gaa ttg cat tca ggt tta gtg aaa atg	1497
Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met	
470 475 480	
caa aag acc att aaa gac aag ctc act acc atg agc ggg gct ttt gat	1545
Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp	
485 490 495	
tgc ctc atg ccc cat gac ttg gtc aat tct aaa atg atc aca agc acc	1593
Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr	
500 505 510 515	
atc atg gaa ttt ttc atg ggc ggt cag ctc tgc caa ttt atg gat caa	1641
Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe Met Asp Gln	
520 525 530	
acg aat ccc ttg agt gag gtt acg cac aag cgc cgc ctt tca gcg ctc	1689
Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu Ser Ala Leu	
535 540 545	
ggc gaa ggg ggg ttg gtg aaa gac aga gtg ggg ttt gaa gcc agg gat	1737
Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu Ala Arg Asp	
550 555 560	
gtg cac ccc acg cat tat ggc cga att tgt ccc att gag acc cca gaa	1785
Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu	
565 570 575	
ggc caa aat atc ggt ctg atc aac acc ctt tcc act ttc aca aga gtg	1833
Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe Thr Arg Val	
580 585 590 595	
aat gat tta ggc ttt att gaa gcc cct tat aaa aag gtt gtg gat ggc	1881
Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val Val Asp Gly	
600 605 610	
aag gtc gtg ggt gag acg att tat ttg acc gct att caa gaa gac agc	1929
Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln Glu Asp Ser	
615 620 625	
cac atc atc gct ccc gca agc acc ccc att gat gaa gag ggg aat att	1977
His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu Gly Asn Ile	
630 635 640	
ttg ggc gat ttg att gaa acg cgc gtg gaa ggc gag atc gtt tta aac	2025
Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile Val Leu Asn	
645 650 655	
gaa aaa agc aaa gta acc tta atg gat tta agc tct agc atg cta gtg	2073
Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser Met Leu Val	
660 665 670 675	

ggg gta gcc gca tcg ctc att cct ttc tta gag cat gat gac gcc aac	2121
Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn	
680 685 690	
cggt gcc tta atg ggg act aac atg cag cgc caa gcg gtg ccc tta tta	2169
Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val Pro Leu Leu	
695 700 705	
aga agc gac gct ccc att gta ggc acg ggg att gaa aaa att att gct	2217
Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala	
710 715 720	
agg gat tct tgg gga gcg atc aaa gcc aat cgc gca ggc gtt gta gaa	2265
Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu	
725 730 735	
aaa att gat tct aaa aat att tat att tta ggc gaa agc aaa gaa gaa	2313
Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu	
740 745 750 755	
gcc tat att gat gcg tat tct ttg caa aaa aac ttg cgc acc aac caa	2361
Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln	
760 765 770	
aac acc agt ttc aat caa gtc cct atc gtt aaa gtg ggc gat aaa gtg	2409
Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val	
775 780 785	
gga gcc ggg caa atc atc gct gat ggc cct agc atg gat aga ggc gag	2457
Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu	
790 795 800	
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Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly	
805 810 815	
tat aac ttt gaa gac gcg atc gtg gtg agt gag tgc atc act aaa gat	2553
Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp	
820 825 830 835	
gat att ttc act tcc acc cac att tat gaa aaa gaa gtg gat gct agg	2601
Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg	
840 845 850	
gag ctt aag cat ggt gtg gaa gaa ttt acc gct gat att cct gat gtg	2649
Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val	
855 860 865	
aaa gaa gaa gcg ctc gct cat ctt gat gaa agc ggg atc gtt aaa gtc	2697
Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val	
870 875 880	
ggt act tat gtg agc gct ggc atg att ttg gtg ggc aaa act tct cct	2745
Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro	

885	890	895	
aaa ggc gag att	aaa agc acg cct	gaa gag cgg ctt	tta agg gct att 2793
Lys Gly Glu Ile	Lys Ser Thr Pro	Glu Glu Arg Leu	Leu Arg Ala Ile
900	905	910	915
ttt ggg gat aaa	gcc ggg cat gtg	gtc aat aag agt	ttg tat tgc cct 2841
Phe Gly Asp Lys	Ala Gly His Val	Val Asn Lys Ser	Leu Tyr Cys Pro
	920	925	930
ccc agt ttg gaa	ggc acg gtg att	gat gtg aaa gtc	ttc act aaa aaa 2889
Pro Ser Leu Glu	Gly Thr Val Ile	Asp Val Lys Val	Phe Thr Lys Lys
	935	940	945
ggc tat gag aaa	gac gcg cga gtt	ttg agc gcg tat	gaa gaa gaa aaa 2937
Gly Tyr Glu Lys	Asp Ala Arg Val	Leu Ser Ala Tyr	Glu Glu Glu Lys
	950	955	960
gcc aag ctt gat	atg gag cat ttt	gat cgc ttg acc	atg ctc aat aga 2985
Ala Lys Leu Asp	Met Glu His Phe	Asp Arg Leu Thr	Met Leu Asn Arg
	965	970	975
gaa gaa ttg ttg	cgc gtt act cgc	tcc ttt ctc aag	cga ttt 3027
Glu Glu Leu Leu	Arg Val Thr Arg	Ser Phe Leu Lys	Arg Phe
980	985	990	
tagaagagcc tttcagccat aacggcaagg attataaaga aggcgatcaa atcccta			3084
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<213> Helicobacter pylori			
<400> 80			
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1	5	10	15
Lys Thr Pro Thr	Asp Leu Glu Val	Pro Asn Leu Leu	Leu Leu Gln Arg
	20	25	30
Asp Ser Tyr Asp	Ser Phe Leu Tyr	Ser Lys Glu Gly	Lys Glu Ser Gly
	35	40	45
Ile Glu Lys Val	Phe Lys Ser Ile	Phe Pro Ile Gln	Asp Glu His Asn
	50	55	60
Arg Ile Thr Leu	Glu Tyr Ala Gly	Cys Glu Phe Gly	Lys Ser Lys Tyr
65	70	75	80
Thr Val Arg Glu	Ala Met Glu Arg	Gly Ile Thr Tyr	Ser Ile Pro Leu
	85	90	95
Lys Ile Lys Val	Arg Leu Ile Leu	Trp Glu Lys Asp	Thr Lys Ser Gly
	100	105	110
Glu Lys Asn Gly	Ile Lys Asp Ile	Lys Glu Gln Ser	Ile Phe Ile Arg
	115	120	125
Glu Ile Pro Leu	Met Thr Glu Arg	Thr Ser Phe Ile	Ile Asn Gly Val
	130	135	140
Glu Arg Val Val	Val Asn Gln Leu	His Arg Ser Pro	Gly Val Ile Phe
145	150	155	160
Lys Glu Glu Glu	Ser Ser Thr Ser	Leu Asn Lys Leu	Ile Tyr Thr Gly

Val	Asp	Gly	Lys	Val	Val	Gly	Glu	Thr	Ile	Tyr	Leu	Thr	Ala	Ile	Gln
610						615					620				
Glu	Asp	Ser	His	Ile	Ile	Ala	Pro	Ala	Ser	Thr	Pro	Ile	Asp	Glu	Glu
625					630					635					640
Gly	Asn	Ile	Leu	Gly	Asp	Leu	Ile	Glu	Thr	Arg	Val	Glu	Gly	Glu	Ile
				645					650					655	
Val	Leu	Asn	Glu	Lys	Ser	Lys	Val	Thr	Leu	Met	Asp	Leu	Ser	Ser	Ser
			660					665					670		
Met	Leu	Val	Gly	Val	Ala	Ala	Ser	Leu	Ile	Pro	Phe	Leu	Glu	His	Asp
		675					680					685			
Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Thr	Asn	Met	Gln	Arg	Gln	Ala	Val
	690					695					700				
Pro	Leu	Leu	Arg	Ser	Asp	Ala	Pro	Ile	Val	Gly	Thr	Gly	Ile	Glu	Lys
705					710					715					720
Ile	Ile	Ala	Arg	Asp	Ser	Trp	Gly	Ala	Ile	Lys	Ala	Asn	Arg	Ala	Gly
				725					730					735	
Val	Val	Glu	Lys	Ile	Asp	Ser	Lys	Asn	Ile	Tyr	Ile	Leu	Gly	Glu	Ser
			740					745					750		
Lys	Glu	Glu	Ala	Tyr	Ile	Asp	Ala	Tyr	Ser	Leu	Gln	Lys	Asn	Leu	Arg
		755					760					765			
Thr	Asn	Gln	Asn	Thr	Ser	Phe	Asn	Gln	Val	Pro	Ile	Val	Lys	Val	Gly
	770					775					780				
Asp	Lys	Val	Gly	Ala	Gly	Gln	Ile	Ile	Ala	Asp	Gly	Pro	Ser	Met	Asp
785					790					795					800
Arg	Gly	Glu	Leu	Ala	Leu	Gly	Lys	Asn	Val	Arg	Val	Ala	Phe	Met	Pro
				805					810					815	
Trp	Asn	Gly	Tyr	Asn	Phe	Glu	Asp	Ala	Ile	Val	Val	Ser	Glu	Cys	Ile
		820						825					830		
Thr	Lys	Asp	Asp	Ile	Phe	Thr	Ser	Thr	His	Ile	Tyr	Glu	Lys	Glu	Val
	835						840					845			
Asp	Ala	Arg	Glu	Leu	Lys	His	Gly	Val	Glu	Glu	Phe	Thr	Ala	Asp	Ile
	850				855						860				
Pro	Asp	Val	Lys	Glu	Glu	Ala	Leu	Ala	His	Leu	Asp	Glu	Ser	Gly	Ile
865					870					875					880
Val	Lys	Val	Gly	Thr	Tyr	Val	Ser	Ala	Gly	Met	Ile	Leu	Val	Gly	Lys
			885						890					895	
Thr	Ser	Pro	Lys	Gly	Glu	Ile	Lys	Ser	Thr	Pro	Glu	Glu	Arg	Leu	Leu
			900					905					910		
Arg	Ala	Ile	Phe	Gly	Asp	Lys	Ala	Gly	His	Val	Val	Asn	Lys	Ser	Leu
	915						920					925			
Tyr	Cys	Pro	Pro	Ser	Leu	Glu	Gly	Thr	Val	Ile	Asp	Val	Lys	Val	Phe
	930					935					940				
Thr	Lys	Lys	Gly	Tyr	Glu	Lys	Asp	Ala	Arg	Val	Leu	Ser	Ala	Tyr	Glu
945					950					955					960
Glu	Glu	Lys	Ala	Lys	Leu	Asp	Met	Glu	His	Phe	Asp	Arg	Leu	Thr	Met
				965					970					975	
Leu	Asn	Arg	Glu	Glu	Leu	Leu	Arg	Val	Thr	Arg	Ser	Phe	Leu	Lys	Arg
			980					985					990		
Phe															

<210> 81
 <211> 581
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(525)

<400> 81

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                                     Met His Ser
                                     1

cca aat tta gaa aaa gaa gaa acc gaa atc ata gaa aca ctc ctt atg 105
Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr Leu Leu Met
   5              10              15

cgt gaa aaa atg cgt tta tgc ccc ttg tat tgg cgc atc tta gcg ttt 153
Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe
  20              25              30              35

tta acc gat ggt ttg tta gtg gcg ttt tta ttg agc gat ctt tta gac 201
Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp
              40              45              50

gca tgc gat ttc ttg cat tct tta tat tgg cta gct aac cct att tat 249
Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr
              55              60              65

cac agc gca ttt gtt gcg atg ggt ttt atc atc ttg tat ggc gtt tat 297
His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr
              70              75              80

gaa atc ttt ttt gtg tgt ttg tgc aag atg agc ttg gct aaa ctg gtt 345
Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val
   85              90              95

ttt agg att aag att att gat att tat ttg gca gat tgc ccc agt agg 393
Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg
100              105              110              115

gct att tta ttg aag cgt tta ggg tta aag atc gtg gtt ttt cta tgc 441
Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys
              120              125              130

ccc ttt tta tgg ttt gtt gcg ttt aaa aac ccc tat cat agg gcg tgg 489
Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp
              135              140              145

cat gaa gaa aaa agc aaa agt ctt ttg gta ttg ttt taatcatgat 535
His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
   150              155

ttattggttg tatttggcgg tctttttttt gttgagcgca ttagac 581
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<210> 82

<211> 159

<212> PRT
 <213> Helicobacter pylori

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 Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile
 20 25 30
 Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp
 35 40 45
 Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn
 50 55 60
 Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr
 65 70 75 80
 Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala
 85 90 95
 Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys
 100 105 110
 Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val
 115 120 125
 Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His
 130 135 140
 Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
 145 150 155

<210> 83
 <211> 901
 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (67)...(852)

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 tttaaa atg agg tat caa aac atg ttt gaa acc tta aaa aaa cac gaa 108
 Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu
 1 5 10
 aaa atg gcg ttt atc ccg ttt gta acc ttg ggc gat cct aat tat gaa 156
 Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu
 15 20 25 30
 ttg agt ttt gaa atc att aaa acc cta att att agc ggg gtg agc gct 204
 Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala
 35 40 45
 tta gaa ttg ggt ctt gct ttt tct gat cct gtg gcg gat ggc att acc 252
 Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr
 50 55 60
 ata caa gcg agc cat tta agg gcg tta aaa cac gct agc atg gct aaa 300
 Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys

65	70	75	
aat ttc cag ctt tta aaa aag att aga gat tac aac cac aat att ccc			348
Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro			
80	85	90	
ata ggg ctt tta gcg tat gcg aat tta att ttt tct tat ggc gtt gat			396
Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp			
95	100	105	110
ggc ttt tac gct caa gct aaa gaa tgc ggt ata gat agc gtt tta ata			444
Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile			
	115	120	125
gcg gac atg ccc cta ata gaa aaa gaa tta gtc atc aaa tcc gct caa			492
Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln			
	130	135	140
aaa cac caa atc aag caa atc ttt atc gcc agc ccc aat gcg agc agt			540
Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser			
	145	150	155
aaa gat tta gaa caa gtc gct acg cat tcg caa ggc tat atc tac gct			588
Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala			
160	165	170	
tta gcc agg agt ggg gtt aca ggg gcg agc cgt att tta gag aat gat			636
Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp			
175	180	185	190
tcg agt gct att att aaa acc tta aaa gct ttt agc cct acc cca gcc			684
Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala			
	195	200	205
tta ctg ggc ttt ggc att tcc aaa aaa gaa cac atc aca aac gct aaa			732
Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys			
	210	215	220
ggc atg ggt gct gat ggc gtg att tgc gga tca gcg tta gtc aaa atc			780
Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile			
225	230	235	
ata gaa gaa aat tta aac aat gaa aac gcc atg ctg gaa aaa att aaa			828
Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys			
240	245	250	
ggg ttt ata gga gga atg att ttt taaggctttt aggcttttggt gcgttaaaaa			882
Gly Phe Ile Gly Gly Met Ile Phe			
255	260		
ttaaagatca cagattaac			901
<210> 84			
<211> 262			
<212> PRT			

<213> Helicobacter pylori

<400> 84

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Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu Lys Met
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Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu Leu Ser
          20          25          30
Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala Leu Glu
          35          40          45
Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr Ile Gln
          50          55          60
Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys Asn Phe
65          70          75          80
Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro Ile Gly
          85          90          95
Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp Gly Phe
          100          105          110
Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile Ala Asp
          115          120          125
Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln Lys His
          130          135          140
Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser Lys Asp
145          150          155          160
Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala Leu Ala
          165          170          175
Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp Ser Ser
          180          185          190
Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala Leu Leu
          195          200          205
Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys Gly Met
          210          215          220
Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile Ile Glu
225          230          235          240
Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys Gly Phe
          245          250          255
Ile Gly Gly Met Ile Phe
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<210> 85

<211> 1081

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(954)

<221> misc_feature

<222> 919

<223> n = A,T,C or G

<400> 85

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                               Met Asn Lys
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gct att gct agt aag ata ctc atc act ttg ggt ttt tta ttt ctc tac	105
Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu Phe Leu Tyr	
5 10 15	
aga gtc tta gct tat atc ccc att cct ggc gta gat tta gca gcg atc	153
Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu Ala Ala Ile	
20 25 30 35	
aag gct ttt ttt gac agc aat tcc aac aac gct ttg ggg ttg ttt aat	201
Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly Leu Phe Asn	
40 45 50	
atg ttt agc ggg aat gcg gtt tct cgc ttg agc atc atc tcg ttg ggt	249
Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile Ser Leu Gly	
55 60 65	
atc atg ccc tat atc act tct tca att atc atg gag ctt ttg agc gcg	297
Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu Leu Ser Ala	
70 75 80	
act ttc cct aac ctg gct aaa atg aaa aaa gag cgg gat ggc atg caa	345
Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp Gly Met Gln	
85 90 95	
aaa tac atg caa atc gtg cgt tat ttg acc att tta atc acc cta atc	393
Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile Thr Leu Ile	
100 105 110 115	
caa gcg gtg agc gtt tca gta ggc tta agg agc att agt gga gga gcc	441
Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser Gly Gly Ala	
120 125 130	
aat ggg gcg atc atg att gat atg caa gtt ttt atg atc gtt tca gcg	489
Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile Val Ser Ala	
135 140 145	
ttt tct atg ctt aca gga acg atg cta ctc atg tgg ata ggg gag caa	537
Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile Gly Glu Gln	
150 155 160	
atc acg caa agg ggc gtg ggg aat ggg atc agt ctc att att ttt gcc	585
Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile Ile Phe Ala	
165 170 175	
ggg att gtt tca ggg atc cca tca gct att tca ggc aca ttc aat ttg	633
Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr Phe Asn Leu	
180 185 190 195	
gtc aat acg ggc gtt att aat atc tta atg ctc att ggt att gtg ctg	681
Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly Ile Val Leu	
200 205 210	
att gtt tta gcg act att ttt gcg att atc tat gtg gaa tta gct gag	729

Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu Leu Ala Glu
 215 220 225
 cgc agg atc cct att tct tat gcg cgt aaa gtg gtg atg caa aac caa 777
 Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met Gln Asn Gln
 230 235 240
 aac aag cgc atc atg aat tac att cct att aag ttg aat tta agt ggg 825
 Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly
 245 250 255
 gtg atc ccc cct att ttc gct tca gct ttg ctc gtg ttc cct tct acg 873
 Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr
 260 265 270 275
 att ttg cag caa gcc aca agc aac aaa acc ttg caa gcg gtt gcg nat 921
 Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa
 280 285 290
 ttt tta agc ccg caa ggt atg cgt ata ata ttt tgatgttctt gctcatcatc 974
 Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
 295 300
 ttttttgctt actttttattc ttctattgtg ttcaattcta aggatattgc ggataatttg 1034
 aggcgtaatg gcgggtatat tccagggtc aggcctggag aggggac 1081

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 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 291
 <223> Xaa = Any Amino Acid

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 20 25 30
 Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Ala Leu Gly
 35 40 45
 Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile
 50 55 60
 Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu
 65 70 75 80
 Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp
 85 90 95
 Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile
 100 105 110
 Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser
 115 120 125
 Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile
 130 135 140

Val	Ser	Ala	Phe	Ser	Met	Leu	Thr	Gly	Thr	Met	Leu	Leu	Met	Trp	Ile
145					150					155					160
Gly	Glu	Gln	Ile	Thr	Gln	Arg	Gly	Val	Gly	Asn	Gly	Ile	Ser	Leu	Ile
				165					170						175
Ile	Phe	Ala	Gly	Ile	Val	Ser	Gly	Ile	Pro	Ser	Ala	Ile	Ser	Gly	Thr
			180					185					190		
Phe	Asn	Leu	Val	Asn	Thr	Gly	Val	Ile	Asn	Ile	Leu	Met	Leu	Ile	Gly
		195				200					205				
Ile	Val	Leu	Ile	Val	Leu	Ala	Thr	Ile	Phe	Ala	Ile	Ile	Tyr	Val	Glu
	210					215					220				
Leu	Ala	Glu	Arg	Arg	Ile	Pro	Ile	Ser	Tyr	Ala	Arg	Lys	Val	Val	Met
225					230					235					240
Gln	Asn	Gln	Asn	Lys	Arg	Ile	Met	Asn	Tyr	Ile	Pro	Ile	Lys	Leu	Asn
			245					250						255	
Leu	Ser	Gly	Val	Ile	Pro	Pro	Ile	Phe	Ala	Ser	Ala	Leu	Leu	Val	Phe
			260					265					270		
Pro	Ser	Thr	Ile	Leu	Gln	Gln	Ala	Thr	Ser	Asn	Lys	Thr	Leu	Gln	Ala
		275					280					285			
Val	Ala	Xaa	Phe	Leu	Ser	Pro	Gln	Gly	Met	Arg	Ile	Ile	Phe		
	290					295					300				

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 <212> DNA
 <213> Helicobacter pylori

<220>
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 <222> (109) ... (363)

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 Met Arg Phe
 1

tta ttc tct aag act tta ttg atg atg agt tgt tgc aac acc gaa agg 165
 Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn Thr Glu Arg
 5 10 15

atg ttg ttc gtg gtc caa tac aag act aac cct gcc ggg aaa gtg att 213
 Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly Lys Val Ile
 20 25 30 35

aaa aag att gtg aat aat agg ggt aag agt tta aaa atc ttt gct tgc 261
 Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile Phe Ala Cys
 40 45 50

atg gga tcg gtc atg gtg ttt ggc gta acg ctt tgg tgc caa tac ata 309
 Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys Gln Tyr Ile
 55 60 65

gac gct ccc ata aga agc ggt aaa ata aaa tac gga tcc atg atg gat 357
 Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp

70	75	80	
aaa tca tgaatccata agatccactc tgagcttttc aattccacag cggtataaag			413
Lys Ser			
85			
cactctataa			423
<210> 88			
<211> 85			
<212> PRT			
<213> Helicobacter pylori			
<400> 88			
Met Arg Phe Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn			
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Thr Glu Arg Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly			
20 25 30			
Lys Val Ile Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile			
35 40 45			
Phe Ala Cys Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys			
50 55 60			
Gln Tyr Ile Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser			
65 70 75 80			
Met Met Asp Lys Ser			
85			
<210> 89			
<211> 740			
<212> DNA			
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<221> CDS			
<222> (59)...(688)			
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atg tta ttg aaa aca aaa tta aaa att ata agc tcg gtg att ttg agc			106
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser			
1 5 10 15			
gct tta ttg tgg gtg ggt tgc tca agc gaa atg gca act tat caa aac			154
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn			
20 25 30			
gtg aat gat gcc act aaa aat acg act gca agc att aat agc acg gat			202
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp			
35 40 45			
tta ttg cta acc gct aac gcg atg tta gat tcc atg ttt agc gac cct			250
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro			
50 55 60			

aat ttt gag caa ctc aag ggc aag cat ttg att gaa gtt tca gat gtg 298
 Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val
 65 70 75 80
 att aac gac acc acg cag ccc aat ttg gac atg aat ctt ttg acg act 346
 Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr
 85 90 95
 gaa atc gcg cgg cag ttg cgg ttg cga tct aat ggg agg ttc aat atc 394
 Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile
 100 105 110
 aca agg gcg agc gga ggg agt ggc att gca gcc gat agc aga atg gtg 442
 Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val
 115 120 125
 aaa cag cgc gaa aaa gaa cga gag agc gaa gag tat aat caa gac acc 490
 Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr
 130 135 140
 act gta gaa aaa ggc act tta aaa gcc gct gat tta tct tta agt ggt 538
 Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly
 145 150 155 160
 aaa gta tct agt atc gca gcc tct att agt agt tct agg cag cgc ttg 586
 Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu
 165 170 175
 gac tat gac ttc acc cta agc ctt acc aac agg aaa acg ggt gaa gag 634
 Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu
 180 185 190
 gta tgg agc gat gtt aag cct att gtg aag aac gct agc aat aag cgt 682
 Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg
 195 200 205
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 Met Phe
 210

tt 740

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 <212> PRT
 <213> Helicobacter pylori

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 20 25 30
 Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp
 35 40 45
 Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro

Ser	Leu	Asn	Ile	Glu	Leu	Cys	Asn	Val	Ser	Glu	Asn	Asn	Ala	Cys	Ala	
75					80					85					90	
ttg	aaa	gtg	gtt	aaa	gac	tgg	ctt	gaa	aaa	gaa	gag	gat	tta	gag	tct	401
Leu	Lys	Val	Val	Lys	Asp	Trp	Leu	Glu	Lys	Glu	Glu	Asp	Leu	Glu	Ser	
				95					100					105		
aaa	aaa	gcg	ggc	aaa	cac	tac	gaa	ctt	ttg	atc	act	aaa	ttg	ggg	aag	449
Lys	Lys	Ala	Gly	Lys	His	Tyr	Glu	Leu	Leu	Ile	Thr	Lys	Leu	Gly	Lys	
			110					115					120			
agt	atc	gta	gag	act	tat	aat	acc	ttt	tta	aac	gca	ttc	aat	ttt	tgc	497
Ser	Ile	Val	Glu	Thr	Tyr	Asn	Thr	Phe	Leu	Asn	Ala	Phe	Asn	Phe	Cys	
		125					130					135				
ggc	atg	att	tta	ttc	tac	ttc	att	aaa	agc	gtt	ttc	aac	ccc	aaa	cgc	545
Gly	Met	Ile	Leu	Phe	Tyr	Phe	Ile	Lys	Ser	Val	Phe	Asn	Pro	Lys	Arg	
	140					145					150					
ttt	tgt	atc	act	cct	ttg	ctc	tat	cat	atc	aat	gaa	tcc	ggg	ttt	aag	593
Phe	Cys	Ile	Thr	Pro	Leu	Leu	Tyr	His	Ile	Asn	Glu	Ser	Gly	Phe	Lys	
155					160					165					170	
gtt	ttg	cca	gtg	agt	att	tta	acg	gtg	ttt	atc	gtg	ggg	ttt	gcc	gtt	641
Val	Leu	Pro	Val	Ser	Ile	Leu	Thr	Val	Phe	Ile	Val	Gly	Phe	Ala	Val	
				175					180					185		
gct	tta	caa	ggg	gct	tta	caa	tta	caa	gac	atg	ggc	gcg	cct	tta	atg	689
Ala	Leu	Gln	Gly	Ala	Leu	Gln	Leu	Gln	Asp	Met	Gly	Ala	Pro	Leu	Met	
			190					195					200			
tcg	gtg	gaa	atg	acg	gct	aaa	ctc	gct	tta	aga	gaa	atc	ggc	cct	ttt	737
Ser	Val	Glu	Met	Thr	Ala	Lys	Leu	Ala	Leu	Arg	Glu	Ile	Gly	Pro	Phe	
		205					210					215				
att	tta	acc	ctt	gtg	gtg	gcc	ggg	agg	agc	gcg	agc	agt	ttt	acc	gcg	785
Ile	Leu	Thr	Leu	Val	Val	Ala	Gly	Arg	Ser	Ala	Ser	Ser	Phe	Thr	Ala	
	220					225					230					
caa	att	ggg	gtg	atg	aag	atc	act	gag	gaa	tta	gac	gcg	atg	aaa	acc	833
Gln	Ile	Gly	Val	Met	Lys	Ile	Thr	Glu	Glu	Leu	Asp	Ala	Met	Lys	Thr	
235					240					245				250		
atg	ggc	ttt	aac	cct	ttt	gaa	ttt	tta	gtg	ttg	cct	agg	gtg	tta	gcc	881
Met	Gly	Phe	Asn	Pro	Phe	Glu	Phe	Leu	Val	Leu	Pro	Arg	Val	Leu	Ala	
				255					260					265		
tta	gtg	att	gtt	ttg	cct	tta	ttg	gtg	ttt	att	gcc	gat	gcg	ttc	gcc	929
Leu	Val	Ile	Val	Leu	Pro	Leu	Leu	Val	Phe	Ile	Ala	Asp	Ala	Phe	Ala	
			270					275					280			
att	ctt	ggg	ggc	atg	ttt	gcg	att	aaa	tac	caa	ttg	gat	tta	ggc	ttc	977
Ile	Leu	Gly	Gly	Met	Phe	Ala	Ile	Lys	Tyr	Gln	Leu	Asp	Leu	Gly	Phe	
		285					290					295				

ccg agc tat att gac aga ttc cat gac aca gtg ggt tgg aac cat ttt 1025
 Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe
 300 305 310

ttg gta ggg att gtc aaa gcc cct ttt tgg ggg ttt gcg att gcg atg 1073
 Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met
 315 320 325 330

gta ggg tgc atg cgc ggg ttt gaa gtc aag ggg gat act gag agc att 1121
 Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile
 335 340 345

ggg cgc ttg acc act att agc gtc gtg aac gct ttg ttt tgg atc att 1169
 Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile
 350 355 360

ttc tta gac gct att ttt tct atc atc ttt tct aag ttg aac ata 1214
 Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile
 365 370 375

taatgaacgc tactaacaat caagtcttaa ttgaagtga ggatctccat agcgc 1269

<210> 92

<211> 377

<212> PRT

<213> Helicobacter pylori

<400> 92

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 20 25 30
 Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu Leu Asp His Gln Gly Pro
 35 40 45
 Leu Lys Met Asp Phe Ser Gly Cys Gln Lys Val Asp Phe Val Phe Gly
 50 55 60
 Met Phe Leu Phe Asp Leu Val Lys Glu Arg Ser Leu Asn Ile Glu Leu
 65 70 75 80
 Cys Asn Val Ser Glu Asn Asn Ala Cys Ala Leu Lys Val Val Lys Asp
 85 90 95
 Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser Lys Lys Ala Gly Lys His
 100 105 110
 Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys Ser Ile Val Glu Thr Tyr
 115 120 125
 Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys Gly Met Ile Leu Phe Tyr
 130 135 140
 Phe Ile Lys Ser Val Phe Asn Pro Lys Arg Phe Cys Ile Thr Pro Leu
 145 150 155 160
 Leu Tyr His Ile Asn Glu Ser Gly Phe Lys Val Leu Pro Val Ser Ile
 165 170 175
 Leu Thr Val Phe Ile Val Gly Phe Ala Val Ala Leu Gln Gly Ala Leu
 180 185 190
 Gln Leu Gln Asp Met Gly Ala Pro Leu Met Ser Val Glu Met Thr Ala
 195 200 205
 Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe Ile Leu Thr Leu Val Val

210	215	220
Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala Gln Ile Gly Val Met Lys		
225	230	235
Ile Thr Glu Glu Leu Asp Ala Met Lys Thr Met Gly Phe Asn Pro Phe		
	245	250
Glu Phe Leu Val Leu Pro Arg Val Leu Ala Leu Val Ile Val Leu Pro		
	260	265
Leu Leu Val Phe Ile Ala Asp Ala Phe Ala Ile Leu Gly Gly Met Phe		
	275	280
Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe Pro Ser Tyr Ile Asp Arg		
	290	295
Phe His Asp Thr Val Gly Trp Asn His Phe Leu Val Gly Ile Val Lys		
305	310	315
Ala Pro Phe Trp Gly Phe Ala Ile Ala Met Val Gly Cys Met Arg Gly		
	325	330
Phe Glu Val Lys Gly Asp Thr Glu Ser Ile Gly Arg Leu Thr Thr Ile		
	340	345
Ser Val Val Asn Ala Leu Phe Trp Ile Ile Phe Leu Asp Ala Ile Phe		
	355	360
Ser Ile Ile Phe Ser Lys Leu Asn Ile		
370	375	

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 <213> *Helicobacter pylori*

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 Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1 5 10 15

 ata gcg gtc att tcg tgg atg gca gcg ttg ttt tat ttg ccg cgc ctt 155
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
 20 25 30

 ttt gtc tat cat gca gaa aac gcg cat aaa aaa gag ttt gta gga gtg 203
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35 40 45

 gtt caa atc caa gaa aaa aag ctt tat tcc ttt atc gct tca ccg gct 251
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50 55 60

 atg ggt ttt acg ctt att aca ggg att tta atg ctg ttg ata gag cct 299
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
 65 70 75 80

 acg ctc ttt aaa agt ggg ggt tgg ttg cat gct aaa ttg gct tta gtg 347

Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
 85 90 95

gtt tta ctt tta gcc tat cat ttt tat tgc aaa aaa tgc atg cgc gag 395
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
 100 105 110

ctg gaa aaa gac ccc aca agg aga aac gca agg ttt tat cgc gtg ttt 443
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
 115 120 125

aat gag gcg cca acg att tta atg atc ctc att gtg att tta gtg gtt 491
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
 130 135 140

gtc aag cct ttt taaagacaag ccatgaaaaa agaaaagtca tgaaaaaaga 543
 Val Lys Pro Phe
 145

aaagcatctc aagc 557

<210> 94
 <211> 148
 <212> PRT
 <213> Helicobacter pylori

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 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
 20 25 30
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35 40 45
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50 55 60
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
 65 70 75 80
 Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
 85 90 95
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
 100 105 110
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
 115 120 125
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
 130 135 140
 Val Lys Pro Phe
 145

<210> 95
 <211> 1671
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (50)...(1624)

<400> 95

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Met Lys Leu

1

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Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu Leu Gly Val
5 10 15

ggg ttt tct gtg cct tct tta cta gaa act aaa ggc cct aaa atc act 154
Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro Lys Ile Thr
20 25 30 35

tta ggt ttg gat tta agg ggg ggg ttg aac atg ctt tta ggg gta caa 202
Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu Gly Val Gln
40 45 50

acc gat gag gct tta aaa aac aag tat tta agc ttg gcg tcc gct tta 250
Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala Ser Ala Leu
55 60 65

gaa tac aac gct aaa aag caa aat atc ttg ctt aaa gat att aaa tcc 298
Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp Ile Lys Ser
70 75 80

aat tta gaa ggg atc agt ttt gag ctt tta gat gaa gat gaa gcg aaa 346
Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp Glu Ala Lys
85 90 95

aaa tta gac gcg ctt tta ttg gaa ttg caa ggc cat agc cag ttt gaa 394
Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser Gln Phe Glu
100 105 110 115

atc aaa aag gaa gcg ggg ttt tat agc gtg aat ctc acc cct tta gag 442
Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr Pro Leu Glu
120 125 130

caa gaa gaa ttg cgt aaa aac acg att ttg caa gtg ata ggg atc att 490
Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile Gly Ile Ile
135 140 145

cgt aac cgc ttg gat caa ttt ggt ttg gca gag cct gta gtc att cag 538
Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val Val Ile Gln
150 155 160

caa ggt aaa gaa gaa att ttc gtg caa ttg cct ggc att aag act tta 586
Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile Lys Thr Leu
165 170 175

gaa gaa gaa cgg cgc gct aaa gac ttg att tca aga tcc gct cat ttg 634
Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser Ala His Leu
180 185 190 195

cag atg atg gcg gtg gat gaa gaa cac aat aaa gat gcg atg aaa atg	682
Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala Met Lys Met	
200 205 210	
acg gat tta gag gct caa aaa tta ggc agc gtg ttg ttg tct gat gtg	730
Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu Ser Asp Val	
215 220 225	
gaa atg ggg ggt aaa atc ttg ctc aaa gcg atc ccc att tta gat ggc	778
Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile Leu Asp Gly	
230 235 240	
gaa atg ctt aca gat gcg aaa gtg gtg tat gac caa aac aac cag ccg	826
Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn Asn Gln Pro	
245 250 255	
gtg gtg agc ttc acg ctg gat gcg caa ggg gct aag att ttt ggg gat	874
Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile Phe Gly Asp	
260 265 270 275	
ttc tca ggt gcg aat gtg ggc aaa cgc atg gcg att gtt tta gac aat	922
Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val Leu Asp Asn	
280 285 290	
aag gtc tat tca gcc ccg gtg att agg gag cgt atc ggt ggg ggg agc	970
Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser	
295 300 305	
ggg cag att agc ggg aat ttt agc gtg gct caa gcg agc gat tta gcg	1018
Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala	
310 315 320	
atc gct tta agg agt ggg gcg atg agc gct ccc att cag gtt tta gaa	1066
Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu	
325 330 335	
aaa aga att ata ggc cca agt tta ggg aaa gac agc gtt aaa act tcc	1114
Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser	
340 345 350 355	
att atc gct cta gtt ggg ggc ttt att tta gtg atg ggc ttt atg gtg	1162
Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val	
360 365 370	
ctt tat tac tct atg gcg ggg gtg atc gct tgt ttg gcg tta gtg gtc	1210
Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val	
375 380 385	
aat ctt ttt ttg att gtg gcg gtc atg gcg att ttt gga gcg acg ctg	1258
Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu	
390 395 400	
act tta ccg gga atg gcg ggg att gtt tta acc gtg ggg att gcc gtg	1306
Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val	

405	410	415	
gat gct aat atc atc atc aac gag cgc att aga gaa gtc tta aga gag			1354
Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu			
420	425	430	435
aat gag ggc atc gct aaa gcg atc cat tta ggc tat atc aat gcg agc			1402
Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser			
	440	445	450
cgg gcg att ttt gat tct aat atc act tct ttg atc gct tca gtg tta			1450
Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu			
	455	460	465
tta tac gct tat ggc aca gga gcg att aaa ggc ttt gcc cta act aca			1498
Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr			
	470	475	480
ggc att ggg att tta gcc tct att atc acc gct att gtt ggc acg caa			1546
Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln			
	485	490	495
ggg att tat caa gcc ctt tta cct aaa ctc act caa aca aaa agc ctt			1594
Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu			
500	505	510	515
tac ttt tgg ttt ggc gtg aat aaa aga gct taggaggttt tatggaatta			1644
Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala			
	520	525	
ttcaaacgaa ctagaatctt aagcttc			1671
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<212> PRT			
<213> Helicobacter pylori			
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Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro			
	20	25	30
Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu			
	35	40	45
Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala			
	50	55	60
Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp			
65	70	75	80
Ile Lys Ser Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp			
	85	90	95
Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser			
	100	105	110
Gln Phe Glu Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr			
	115	120	125
Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile			

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<221> CDS

<222> (64)...(654)

<400> 97

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  Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe
    1             5             10             15

gta gtt ttg tct ttc att acg ata gga tta gtg ttt ttc ttt ttg cgt 156
Val Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg
          20             25             30

tcc caa ccc act agc gta gtt tct aaa gaa aat atc cct aaa att gaa 204
Ser Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu
          35             40             45

tta gaa aat ttt aaa gcg ttt caa atc aac gat aaa atc ctt gat ctg 252
Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu
          50             55             60

tcc ata gag ggc aaa aaa gcc cta caa tac gat gat cat gaa atc ttt 300
Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe
          65             70             75

ttt gat tcc aaa atc aag cgc tat gat gaa gac acc att gaa agc gtt 348
Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val
          80             85             90             95

gag tct cct aag gcc aaa cgg cag cag gat ttg tat ttc ttc cct aat 396
Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn
          100            105            110

ggg gtt act tat aaa aga agc gat gat tcc agt ttt tgg agt gaa aca 444
Gly Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr
          115            120            125

ggg att tat aac cat aag gag caa aat ttt aaa ggc aag ggc cgt ttc 492
Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe
          130            135            140

att ctc act tca aag gac agc aag att gaa ggg ctt gac att tct tat 540
Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr
          145            150            155

tcg cat gca tta gct att att gaa gct caa agc att caa gcg cat tta 588
Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu
          160            165            170            175

ttc tta gat gaa atc aaa caa agc caa aaa gaa aag aaa aaa ttc ccc 636
Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro
          180            185            190

act ttc aaa gga ggt ttt taatgcgttg gtggtgtttt ttggtgtgtt 684
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Thr Phe Lys Gly Gly Phe
195

gttttggtat tttaagcgtg at

706

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<211> 197
<212> PRT
<213> Helicobacter pylori

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Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe Val
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20 25 30
Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu Leu
35 40 45
Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu Ser
50 55 60
Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe Phe
65 70 75 80
Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val Glu
85 90 95
Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn Gly
100 105 110
Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr Gly
115 120 125
Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile
130 135 140
Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr Ser
145 150 155 160
His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu Phe
165 170 175
Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr
180 185 190
Phe Lys Gly Gly Phe
195

<210> 99
<211> 1010
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (130)...(957)

<400> 99
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tttataatta taatTTTtgaa agccatTTTT ttgagccgat tggagaaacc attaaacaaa 120
ggaaaagtc atg aaa act tct aaa aca aaa acc cct aaa tcc gtt tta atc 171
Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile
1 5 10

gct ggg cca tgc gtc att gag agc tta gaa aat cta aga agt atc gcc	219
Ala Gly Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala	
15 20 25 30	
act aaa ttg caa ccc cta gcc aac aac gag cgg ttg gat ttt tat ttt	267
Thr Lys Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe	
35 40 45	
aaa gcg agt ttt gat aag gcg aac cgc acg agt tta gag agt tac aga	315
Lys Ala Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg	
50 55 60	
ggg cct ggt tta gaa aaa ggc cta gaa atg tta caa acg atc aaa gag	363
Gly Pro Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu	
65 70 75	
gaa ttt ggt tat aaa atc tta acc gat gtg cat gag agt tat caa gca	411
Glu Phe Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala	
80 85 90	
agc gtg gca gcc aaa gtg gcg gat att tta caa atc ccg gcg ttt ttg	459
Ser Val Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu	
95 100 105 110	
tgc cgc caa acg gat ctg att gta gaa gtg agc cag act aac gct att	507
Cys Arg Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile	
115 120 125	
gtc aat atc aaa aaa ggg caa ttc atg aac cca aaa gac atg caa tat	555
Val Asn Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr	
130 135 140	
tct gtt cta aag gcc ctt aaa acg aga gat aaa agc att caa agc ccc	603
Ser Val Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro	
145 150 155	
act tat gaa aca gcg tta aaa aat ggc gtg tgg ctg tgt gaa agg ggg	651
Thr Tyr Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly	
160 165 170	
agc agc ttt ggg tat ggg aat tta gtg gtg gat atg cgc tct tta aaa	699
Ser Ser Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys	
175 180 185 190	
atc atg cga gaa ttt gcc cct gtg att ttt gac gct acc cat agc gtg	747
Ile Met Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val	
195 200 205	
caa atg cca ggg gga gcg aac ggg aaa agt tca gga gac agc tct ttt	795
Gln Met Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe	
210 215 220	
gcc cct att tta gcg aga gct gcg gcg gcg gtg ggg att gat ggg ttg	843
Ala Pro Ile Leu Ala Arg Ala Ala Ala Val Gly Ile Asp Gly Leu	
225 230 235	

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ttt gct gaa acg cat gtt gat cct aaa aac gcc cta agc gat gga gca 891
Phe Ala Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala
240 245 250

aac atg cta aaa cct gac gag cta gaa caa tta gta acc gac atg tta 939
Asn Met Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu
255 260 265 270

aaa atc caa aat tta ttt taaaggaatt tcatgcaaat catagaaggg 987
Lys Ile Gln Asn Leu Phe
275

aaattgcaat tacaagggaa tga 1010

<210> 100
<211> 276
<212> PRT
<213> Helicobacter pylori

<400> 100
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1 5 10 15
Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala Thr Lys
20 25 30
Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe Lys Ala
35 40 45
Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg Gly Pro
50 55 60
Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu Glu Phe
65 70 75 80
Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala Ser Val
85 90 95
Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu Cys Arg
100 105 110
Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile Val Asn
115 120 125
Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr Ser Val
130 135 140
Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro Thr Tyr
145 150 155 160
Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly Ser Ser
165 170 175
Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys Ile Met
180 185 190
Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val Gln Met
195 200 205
Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe Ala Pro
210 215 220
Ile Leu Ala Arg Ala Ala Ala Val Gly Ile Asp Gly Leu Phe Ala
225 230 235 240
Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn Met
245 250 255
Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu Lys Ile
260 265 270

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Gln Asn Leu Phe
275

<210> 101
<211> 240
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (59)...(196)

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atg aaa ggt cgc gta gct cag ttg gta gag cac tac ctt gac atg gta 106
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
1 5 10 15

gtg gcc gct ggt tca agt cca gtc gtg gcc acc att atc act cca att 154
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
20 25 30

tta att ctc att ttt ttg cga gtt ttt gat ctt tat aaa ttc 196
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
35 40 45

taaaggggta ttaaacgcac ttctaataac gattttatag cgct 240

<210> 102
<211> 46
<212> PRT
<213> Helicobacter pylori

<400> 102
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
1 5 10 15
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
20 25 30
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
35 40 45

<210> 103
<211> 1382
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (91)...(1329)

<400> 103
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tttaacacga taaaagggcg gtttaatagc atg gca caa gaa aaa gca gtt cca 114

	Met	Ala	Gln	Glu	Lys	Ala	Val	Pro	
	1				5				
aga gat cct aaa aaa ctc aat gcg ttt gat ttg cgt tgg atg gtg tcc									162
Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser									
10 15 20									
tta ttt ggc acg gcg gtg ggg gct ggg att tta ttt ttg cct att aga									210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg									
25 30 35 40									
gcc ggt ggg cat ggg gta tgg gct att gtg gta atg agc gcg atc att									258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile									
45 50 55									
ttc cct tta act tat cta ggg cat aga gct tta gct tat ttc ata gga									306
Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly									
60 65 70									
tct aaa gac aaa gaa gac att acc atg gtc gtt cgc tct cat ttt ggc									354
Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly									
75 80 85									
gct caa tgg ggt ttt ctt atc act ttg ctt tat ttc tta gcg att tat									402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr									
90 95 100									
cct att tgc ttg gtt tat ggg gtg ggt atc act aac gtg ttt gat cat									450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His									
105 110 115 120									
ttt ttc act aac cag ttg cat tta gcg cct ttt cat cgg gga tta ttg									498
Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu									
125 130 135									
gct gta gcg tta gtt tct tta atg atg ttg gtg atg gtt ttt aac gct									546
Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala									
140 145 150									
acg att gtt acg cgc att tgt aac gct tta gtg tat cct tta tgc ttg									594
Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu									
155 160 165									
att tta ttg ctt ttt tct ttg tat ctt atc cct tat tgg caa ggc gct									642
Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala									
170 175 180									
aat ctt ttt gtg gtg ccg agt ttt aaa gaa ttt gtg tta gcg att tgg									690
Asn Leu Phe Val Val Pro Ser Phe Lys Glu Phe Val Leu Ala Ile Trp									
185 190 195 200									
cta acc tta ccg gtg ctt gtg ttt gca ttc gac cat agc ccc atc att									738
Leu Thr Leu Pro Val Leu Val Phe Ala Phe Asp His Ser Pro Ile Ile									
205 210 215									

tca acc ttc act caa aat gtg gga aaa gaa tac ggc gtt ttc aaa gaa	786
Ser Thr Phe Thr Gln Asn Val Gly Lys Glu Tyr Gly Val Phe Lys Glu	
220 225 230	
tac aaa ctc aat caa att gaa tta ggg aca tcg ctg atg ctt tta ggg	834
Tyr Lys Leu Asn Gln Ile Glu Leu Gly Thr Ser Leu Met Leu Leu Gly	
235 240 245	
ttt gtg atg ttt ttt gtg ttt tcg tgc gtc atg tgc ttg aat gct gat	882
Phe Val Met Phe Phe Val Phe Ser Cys Val Met Cys Leu Asn Ala Asp	
250 255 260	
gat ttt gtg aaa gca agg gaa caa aat atc ccc att tta agc tat ttg	930
Asp Phe Val Lys Ala Arg Glu Gln Asn Ile Pro Ile Leu Ser Tyr Leu	
265 270 275 280	
gct aac act tta aac aac cct tta atc aat tat gcg ggg cct gtg gtg	978
Ala Asn Thr Leu Asn Asn Pro Leu Ile Asn Tyr Ala Gly Pro Val Val	
285 290 295	
gct ttt tta gcg att ttt tca tct ttt ttt ggg cat tat tat ggg gct	1026
Ala Phe Leu Ala Ile Phe Ser Ser Phe Phe Gly His Tyr Tyr Gly Ala	
300 305 310	
aag gag ggt tta gaa ggc att att att caa agc tta aaa ttg aaa aaa	1074
Lys Glu Gly Leu Glu Gly Ile Ile Ile Gln Ser Leu Lys Leu Lys Lys	
315 320 325	
gct tct aaa ccc ttg agc gtt agc gta acg att ttt tta tgg ctg act	1122
Ala Ser Lys Pro Leu Ser Val Ser Val Thr Ile Phe Leu Trp Leu Thr	
330 335 340	
atc acg ctt gtg gct tat att aac ccc aat atc ttg gat ttt att gaa	1170
Ile Thr Leu Val Ala Tyr Ile Asn Pro Asn Ile Leu Asp Phe Ile Glu	
345 350 355 360	
aat tta ggc ggc ccc att atc gcg ctc att ctg ttt gtg atg ccc atg	1218
Asn Leu Gly Gly Pro Ile Ile Ala Leu Ile Leu Phe Val Met Pro Met	
365 370 375	
ata gct ttt tat agt gtt tct agt ttg aag cgt ttt aga aat ttc aaa	1266
Ile Ala Phe Tyr Ser Val Ser Ser Leu Lys Arg Phe Arg Asn Phe Lys	
380 385 390	
gtg gat att ttt gtg ttt gtc ttt ggg agc ttg acg gct ttg agc gtg	1314
Val Asp Ile Phe Val Phe Val Phe Gly Ser Leu Thr Ala Leu Ser Val	
395 400 405	
ttt tta gga cta ttt taatggctag tttttctatt ttatctatatt ttaaaatcgg	1369
Phe Leu Gly Leu Phe	
410	
cgtaggggcct agc	1382

<210> 104

<211> 413
 <212> PRT
 <213> Helicobacter pylori

<400> 104
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 1 5 10 15
 Phe Asp Leu Arg Trp Met Val Ser Leu Phe Gly Thr Ala Val Gly Ala
 20 25 30
 Gly Ile Leu Phe Leu Pro Ile Arg Ala Gly Gly His Gly Val Trp Ala
 35 40 45
 Ile Val Val Met Ser Ala Ile Phe Pro Leu Thr Tyr Leu Gly His
 50 55 60
 Arg Ala Leu Ala Tyr Phe Ile Gly Ser Lys Asp Lys Glu Asp Ile Thr
 65 70 75 80
 Met Val Val Arg Ser His Phe Gly Ala Gln Trp Gly Phe Leu Ile Thr
 85 90 95
 Leu Leu Tyr Phe Leu Ala Ile Tyr Pro Ile Cys Leu Val Tyr Gly Val
 100 105 110
 Gly Ile Thr Asn Val Phe Asp His Phe Phe Thr Asn Gln Leu His Leu
 115 120 125
 Ala Pro Phe His Arg Gly Leu Leu Ala Val Ala Leu Val Ser Leu Met
 130 135 140
 Met Leu Val Met Val Phe Asn Ala Thr Ile Val Thr Arg Ile Cys Asn
 145 150 155 160
 Ala Leu Val Tyr Pro Leu Cys Leu Ile Leu Leu Leu Phe Ser Leu Tyr
 165 170 175
 Leu Ile Pro Tyr Trp Gln Gly Ala Asn Leu Phe Val Val Pro Ser Phe
 180 185 190
 Lys Glu Phe Val Leu Ala Ile Trp Leu Thr Leu Pro Val Leu Val Phe
 195 200 205
 Ala Phe Asp His Ser Pro Ile Ile Ser Thr Phe Thr Gln Asn Val Gly
 210 215 220
 Lys Glu Tyr Gly Val Phe Lys Glu Tyr Lys Leu Asn Gln Ile Glu Leu
 225 230 235 240
 Gly Thr Ser Leu Met Leu Leu Gly Phe Val Met Phe Phe Val Phe Ser
 245 250 255
 Cys Val Met Cys Leu Asn Ala Asp Asp Phe Val Lys Ala Arg Glu Gln
 260 265 270
 Asn Ile Pro Ile Leu Ser Tyr Leu Ala Asn Thr Leu Asn Asn Pro Leu
 275 280 285
 Ile Asn Tyr Ala Gly Pro Val Val Ala Phe Leu Ala Ile Phe Ser Ser
 290 295 300
 Phe Phe Gly His Tyr Tyr Gly Ala Lys Glu Gly Leu Glu Gly Ile Ile
 305 310 315 320
 Ile Gln Ser Leu Lys Leu Lys Lys Ala Ser Lys Pro Leu Ser Val Ser
 325 330 335
 Val Thr Ile Phe Leu Trp Leu Thr Ile Thr Leu Val Ala Tyr Ile Asn
 340 345 350
 Pro Asn Ile Leu Asp Phe Ile Glu Asn Leu Gly Gly Pro Ile Ile Ala
 355 360 365
 Leu Ile Leu Phe Val Met Pro Met Ile Ala Phe Tyr Ser Val Ser Ser
 370 375 380
 Leu Lys Arg Phe Arg Asn Phe Lys Val Asp Ile Phe Val Phe Val Phe
 385 390 395 400

Gly Ser Leu Thr Ala Leu Ser Val Phe Leu Gly Leu Phe
405 410

<210> 105
<211> 875
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (63)...(827)

<400> 105
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ga atg cta gat ttt att caa gag ctt agc acc ccc cat gtt agg gat 107
Met Leu Asp Phe Ile Gln Glu Leu Ser Thr Pro His Val Arg Asp
1 5 10 15

ttt ttc ttg ttg ttt tta agg gtt agc ggc gtg ctg tct ttc ttc cct 155
Phe Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro
20 25 30

ttt ttt gaa aac cat tta gtg cct ttg tgc gtg cgt ggg gct ttg agt 203
Phe Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser
35 40 45

ttg tat gtg agc gcg att ttt tac ccc act tta gaa ttt tca aac gcc 251
Leu Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala
50 55 60

gct tac acg cca gag ggt ttt atc att gct tgc ttg tgc gaa ttg ttt 299
Ala Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe
65 70 75

tta ggg gtg tgc gcg tct gtc ttt tta caa atc gtc ttt gca agc tta 347
Leu Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu
80 85 90 95

gtg ttt gca acc gat agc atc agc ttt tct atg ggg ctt acg atg gcg 395
Val Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala
100 105 110

agc gcg tat gat cct att tca gga tgc caa aaa ccc att gtg ggg caa 443
Ser Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln
115 120 125

gcc ctt tta ttg tta gcg att tta att tta ttg gat tta tgc ttc cac 491
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His
130 135 140

cat caa atc att ttg ttt gtg gat cac agc tta aaa gcc gtc cct tta 539
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu
145 150 155

ggg caa ttt gtc ttt gag cca gcg ttg gct aaa aac atc gtt aaa gcc 587
 Gly Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala
 160 165 170 175

 ttt tcg cac ctc ttt gtc ata ggg ttt tct atg gcg ttc cct att tta 635
 Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu
 180 185 190

 tgc ttg gtg tta ttg agc gat att att ttt ggc atg atc atg aaa acc 683
 Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr
 195 200 205

 cac cct cag ttc aac ctg ctc gct att ggg ttt ccg gtt aaa att gcg 731
 His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala
 210 215 220

 atc ggg ttt gtg ggc att atc tta atc gct tcg gct atc atg ggg cgt 779
 Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg
 225 230 235

 ttt aaa gaa gaa atc agc ctg gcc ttt agc gcc att agc aaa atc ttt 827
 Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Ala Ile Ser Lys Ile Phe
 240 245 250 255

 taaaggataa acatgattag ttttaaagaa gctctaaaaa tccattct 875

<210> 106
 <211> 255
 <212> PRT
 <213> Helicobacter pylori

<400> 106
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 1 5 10 15
 Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro Phe
 20 25 30
 Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser Leu
 35 40 45
 Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala Ala
 50 55 60
 Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe Leu
 65 70 75 80
 Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu Val
 85 90 95
 Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala Ser
 100 105 110
 Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln Ala
 115 120 125
 Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His His
 130 135 140
 Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu Gly
 145 150 155 160
 Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala Phe
 165 170 175
 Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu Cys

gta ttt ttg cac gat ctc acc ctt atc att gac aag aat caa agt gtt 747
 Val Phe Leu His Asp Leu Thr Leu Ile Ile Asp Lys Asn Gln Ser Val
 110 115 120 125

 ata ggg att ctt ttt ggc ttg ctc gtg ttt ttc ccc tgt caa aga gaa 795
 Ile Gly Ile Leu Phe Gly Leu Leu Val Phe Phe Pro Cys Gln Arg Glu
 130 135 140

 cac tcc cca aac ctt gtt ttt ctt aca agc ttc agc aaa gat cgc ggt 843
 His Ser Pro Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly
 145 150 155

 ttc ttc tcc agg aac gct tgc ggc tgt atc aaa cat ttc ttg tct gtc 891
 Phe Phe Ser Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val
 160 165 170

 ata cat aat ccc atg cgt gct gta ttc agg gaa aat aat cag atc caa 939
 Ile His Asn Pro Met Arg Ala Val Phe Arg Glu Asn Asn Gln Ile Gln
 175 180 185

 ccc agg caa acc ctg ttt gac ccc acc aat cac ctt agc gat att gcg 987
 Pro Arg Gln Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala
 190 195 200 205

 aca att ttc caa cac ctc att ctt agt gtg gag tct agg cat ctt ata 1035
 Thr Ile Phe Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile
 210 215 220

 att aac tac cgc tac acc cac agt atc tgg gct gct act aat atc tcc 1083
 Ile Asn Tyr Arg Tyr Thr His Ser Ile Trp Ala Ala Thr Asn Ile Ser
 225 230 235

 atg tct cat att atg ttc ctt gtt ttt tgatgagagt tcctacaaac 1130
 Met Ser His Ile Met Phe Leu Val Phe
 240 245

 cctctacttg aatttataaa ataattgtgt 1160

 <210> 108
 <211> 246
 <212> PRT
 <213> Helicobacter pylori

<400> 108
 Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile Gly Ile His
 1 5 10 15
 Pro Ile Lys Thr Gly Arg Ile Arg Tyr Arg Tyr Ile Thr Leu Ile Gly
 20 25 30
 Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Ser Arg Ile
 35 40 45
 His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr His Arg Ala
 50 55 60
 Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn Asn Gln Arg
 65 70 75 80
 Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe Ile Pro Arg

Asp	Phe	Ser	Leu	Leu	Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	
			80						85					90		
att	aaa	gat	tta	cgc	tct	ttc	aaa	gaa	tgg	ata	ccc	tac	cct	tta	agg	399
Ile	Lys	Asp	Leu	Arg	Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	
			95					100					105			
ggg	gct	gtt	atc	act	tct	ggg	aat	att	aaa	ggg	cat	aga	aaa	gcc	ctt	447
Gly	Ala	Val	Ile	Thr	Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	
		110					115					120				
atg	att	caa	ggc	gtc	tct	aat	gtg	gct	caa	tcc	cac	act	gcc	tac	aat	495
Met	Ile	Gln	Gly	Val	Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	
	125					130					135					
gcc	ctt	tta	gat	gat	ttc	aag	ctt	tct	cgc	tta	aat	ttg	aac	gca	caa	543
Ala	Leu	Leu	Asp	Asp	Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	
140					145				150						155	
gac	gcc	aat	tta	gaa	gat	ttg	ctt	tat	tta	atc	aat	cgc	ccc	gct	tat	591
Asp	Ala	Asn	Leu	Glu	Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	
			160					165						170		
gcg	aac	gca	aaa	gtg	tcc	tta	cag	gcg	gat	ttt	aac	tct	cta	aag	cct	639
Ala	Asn	Ala	Lys	Val	Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	
			175					180					185			
tta	gag	ggg	cat	ttg	atc	cta	aca	gct	aat	aac	gct	tta	atc	aat	aac	687
Leu	Glu	Gly	His	Leu	Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	
	190						195					200				
gcc	cta	atc	aat	caa	att	ttt	cat	tta	aac	ctt	aaa	gac	acg	ctt	gtt	735
Ala	Leu	Ile	Asn	Gln	Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	
	205					210					215					
ttc	agc	ctc	tcg	cat	tca	agc	gac	ttt	aaa	gga	aac	aaa	gcc	atc	agc	783
Phe	Ser	Leu	Ser	His	Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	
220					225				230					235		
gat	acc	acc	ctg	act	agc	cct	tta	gcc	aat	ttc	aaa	gcc	cta	aaa	agc	831
Asp	Thr	Thr	Leu	Thr	Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	
			240					245						250		
gaa	tac	ctt	ttc	tct	att	tta	aaa	ctc	aac	gcc	ccc	tac	act	tta	gaa	879
Glu	Tyr	Leu	Phe	Ser	Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	
		255						260					265			
atc	ccc	aat	cta	gcc	aaa	ctc	tat	aac	att	acc	aac	cac	ccc	tta	aaa	927
Ile	Pro	Asn	Leu	Ala	Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	
		270					275					280				
ggg	agc	ttg	act	tta	aaa	ggc	gct	ata	gaa	caa	agc	ccc	aaa	ctt	tta	975
Gly	Ser	Leu	Thr	Leu	Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	
	285					290					295					

aaa gtc agc ggc cat tca aat tta cta gac ggc gcg ctg gat ttc acg	1023
Lys Val Ser Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr	
300 305 310 315	
ctt tta aat aaa gat ttg aaa ggg cgt ttt tcc aat att tcc act tta	1071
Leu Leu Asn Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu	
320 325 330	
aaa gct tta gat tta ttc cat tac cct aag ttt ttc caa tcc gtt gca	1119
Lys Ala Leu Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala	
335 340 345	
gac gct aat ttg gat tat gat ctt atc gct aag caa ggc gta ttg aaa	1167
Asp Ala Asn Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys	
350 355 360	
gcc cgc cta aaa aac gca aga ttc ctc aaa aat gca ttc agc gat ttt	1215
Ala Arg Leu Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe	
365 370 375	
ctc tac tcc att tct aaa ttt gat att aca aaa gaa att tat aac gat	1263
Leu Tyr Ser Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp	
380 385 390 395	
gcc aat ctg gta agc caa atc aac cag caa cgc ctg ctc tct gat ctg	1311
Ala Asn Leu Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu	
400 405 410	
agt tta aaa agc ccc aaa acc caa ttg aaa atc cat aac ggt ttg ttg	1359
Ser Leu Lys Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu	
415 420 425	
gat tta aac acc aaa caa atg aac atg ctc atg gat gcg gaa att tta	1407
Asp Leu Asn Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu	
430 435 440	
aaa ttc att ttt aaa atg aaa ctt caa ggc aac atg cac cag cca aaa	1455
Lys Phe Ile Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys	
445 450 455	
ttt tct ctc att tta aac gaa aaa gcc att cag caa aac ttg caa caa	1503
Phe Ser Leu Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln	
460 465 470 475	
ggc ttg aaa gaa atc tta aaa aac gac acc ctt aaa aaa ggt tta gat	1551
Gly Leu Lys Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp	
480 485 490	
cat ttg ctt aaa gat gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt	1599
His Leu Leu Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu	
495 500 505	
aag ggg ctt ttt taaaatttta aaggatagaa atggcgcaca ttttagttag	1651
Lys Gly Leu Phe	
510	

cggggcgact

1661

<210> 110

<211> 511

<212> PRT

<213> Helicobacter pylori

<400> 110

Met	Lys	Lys	Leu	Leu	Tyr	Thr	Ile	Leu	Ala	Leu	Leu	Leu	Ile	Gly	Leu
1			5					10					15		
Leu	Thr	Ile	Tyr	Leu	Ile	Leu	Phe	Thr	Glu	Trp	Gly	Asn	Lys	Ile	Ile
		20					25					30			
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	His	Tyr	Leu	Ser
		35				40					45				
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
	50					55				60					
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65				70					75					80	
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
			85				90					95			
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr
		100				105						110			
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val
	115					120					125				
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp
	130				135					140					
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu
145				150					155					160	
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val
			165				170					175			
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu
		180					185					190			
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln
	195					200					205				
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His
	210			215						220					
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr
225				230				235						240	
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser
			245				250						255		
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala
		260				265					270				
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu
	275				280						285				
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His
	290				295					300					
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp
305				310				315						320	
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu
			325				330						335		
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp
		340				345						350			
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn
	355					360						365			

Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser
370						375					380				
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser
385					390					395					400
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro
				405					410					415	
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys
			420					425					430		
Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys
	435					440						445			
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu
450					455						460				
Asn	Glu	Lys	Ala	Ile	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile	
465				470				475						480	
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp
			485					490						495	
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe	
		500						505					510		

<210> 111
 <211> 397
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (53)...(352)

<400> 111
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 Met Lys
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aca	aaa	cat	aaa	gga	ata	aga	atg	ttt	aag	caa	att	cgt	aga	atg	atg	106
Thr	Lys	His	Lys	Gly	Ile	Arg	Met	Phe	Lys	Gln	Ile	Arg	Arg	Met	Met	
	5					10						15				

agt	ttg	gca	ata	tta	atg	cct	agt	ttt	tta	ttg	gcg	gca	cca	gat	tac	154
Ser	Leu	Ala	Ile	Leu	Met	Pro	Ser	Phe	Leu	Leu	Ala	Ala	Pro	Asp	Tyr	
	20				25						30					

aaa	caa	aaa	ttc	act	caa	ata	ttg	gat	ttc	ata	agc	aat	gac	ttt	atc	202
Lys	Gln	Lys	Phe	Thr	Gln	Ile	Leu	Asp	Phe	Ile	Ser	Asn	Asp	Phe	Ile	
	35				40				45					50		

aag	gct	att	ggg	ggt	cta	atc	att	ggt	ggg	act	tgc	att	tac	gcc	tat	250
Lys	Ala	Ile	Gly	Gly	Leu	Ile	Ile	Val	Gly	Thr	Cys	Ile	Tyr	Ala	Tyr	
			55					60						65		

aaa	aat	tgg	gac	agg	ctt	gga	gaa	att	ggt	tgg	aaa	tgc	ggt	ggg	att	298
Lys	Asn	Trp	Asp	Arg	Leu	Gly	Glu	Ile	Gly	Trp	Lys	Cys	Val	Gly	Ile	
		70						75					80			

atc	att	ata	acc	gct	gct	att	tct	aat	gct	aaa	act	tta	agt	caa	tgg	346
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Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp
85 90 95

tta ttt tagatggcat tgcattattgt ttgtgttgaa agtatcaaca ttaga 397
Leu Phe
100

<210> 112
<211> 100
<212> PRT
<213> Helicobacter pylori

<400> 112
Met Lys Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg
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Met Met Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro
20 25 30
Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp
35 40 45
Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr
50 55 60
Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val
65 70 75 80
Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser
85 90 95
Gln Trp Leu Phe
100

<210> 113
<211> 367
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (52)...(318)

<400> 113
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Met Ile
1

caa agc gac gct gtc ttt aag ata aat ttc tgt ctt gcc ctt ctt gta 105
Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val
5 10 15

ttt gta aag agg ggc ttg agc gat ata aac atg ccc ttg ttc aat cag 153
Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln
20 25 30

cgg gcg caa ata acg ata gaa aaa agt cat cag caa ggt ttg gat atg 201
Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met
35 40 45 50

20	25	30	
gcc cac aaa aat gag att ttc ttt tgc cct aga aat agc tac att caa			200
Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln			
35	40	45	
gcg ttt aga atc tat caa gaa aga aag att acc ata agt ttt cac ggt			248
Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly			
50	55	60	65
gga ata aat aat aat atc tgc ctt ctc gcc ttg aaa ggc atc cac agt			296
Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser			
70	75	80	
gtc tat ttt gag ctc atc aaa att ctt gaa gcc gta ttt ttc cac ttc			344
Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe			
85	90	95	
tgatcgcaag catctttttt gggcattata aggtgtgata at			386
<210> 116			
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<213> Helicobacter pylori			
<400> 116			
Met Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser			
1	5	10	15
Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu			
20	25	30	
Phe Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile			
35	40	45	
Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His			
50	55	60	
Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His			
65	70	75	80
Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His			
85	90	95	
Phe			
<210> 117			
<211> 569			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (55)...(516)			
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		Ala	
		1	

tca gaa gtg gcc ccc tca gag gtt ttg ttg gat tct tct tgc ttg tct	105
Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser	
5 10 15	
ttt tct ttg act ata tcc tta gtt gtt act tgt tta gga gcg ctt ttt	153
Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe	
20 25 30	
tct tta gct tcc tct tta gct tct tct ttt ttg ggc tct tct tta ggc	201
Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly	
35 40 45	
tct tct ttt tta acc tct tca act tta ggc tca ggc tta ggc tcg ggt	249
Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly	
50 55 60 65	
ttt ggt tca ggt ttg ggt tca ggc tta ggt ttt ggt ttt ggc ttt ggc	297
Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly	
70 75 80	
ttg ggt tta ggc tta ggt tta ggc ttt gta acc tcc ttt ttg ggt tct	345
Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser	
85 90 95	
tct ttt ttt ggc tct tct ttc ttg ggt ttt tct tta ggc tct tct ttg	393
Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu	
100 105 110	
ggt tta gcc gac tca gca tta gtc ttt gta ttg gaa tta gtg ttg atg	441
Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met	
115 120 125	
ctg gct aaa ctc atg gta acc tta gtg gtc ccg gct tgc gct aaa ggc	489
Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly	
130 135 140 145	
tct ggg gcg tct tcg cgc agt aaa aaa tagccaaacc ctatagcgta	536
Ser Gly Ala Ser Ser Arg Ser Lys Lys	
150	
tagggcaaaa gagattaataaa agctaacact cgt	569
<210> 118	
<211> 154	
<212> PRT	
<213> Helicobacter pylori	
<400> 118	
Ala Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu	
1 5 10 15	
Ser Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu	
20 25 30	
Phe Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu	
35 40 45	

Gly Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser
 50 55 60
 Gly Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe
 65 70 75 80
 Gly Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly
 85 90 95
 Ser Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser
 100 105 110
 Leu Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu
 115 120 125
 Met Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys
 130 135 140
 Gly Ser Gly Ala Ser Ser Arg Ser Lys Lys
 145 150

<210> 119
 <211> 359
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (77)...(310)

<400> 119
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 gcatcaaaac cgctac aat gaa cat cat acc cct gca ggc tct ttg gtg tta 112
 Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu
 1 5 10

 gga tct ttt atc atc ggc tct ttt aaa ggc gtg ggt gct ata ggg ggc 160
 Gly Ser Phe Ile Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly
 15 20 25

 gtg ggt gct gtg gtt ttt ggg att tct tta ttt tct ttt ggg ggt ttt 208
 Val Gly Ala Val Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe
 30 35 40

 tgc cac aac tct gtc aaa gcc gcc gct ttt tta gga tcc att ttg gct 256
 Cys His Asn Ser Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala
 45 50 55 60

 aaa att tta ccg agt tct tgg ggt ttt agc gcc att aaa att tct aat 304
 Lys Ile Leu Pro Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn
 65 70 75

 gcg ttt tgagtgggta aattttctaa aatcagagcc gatttagaat ctttcattt 359
 Ala Phe

<210> 120
 <211> 78
 <212> PRT

<213> Helicobacter pylori

<400> 120

Asn	Glu	His	His	Thr	Pro	Ala	Gly	Ser	Leu	Val	Leu	Gly	Ser	Phe	Ile
1				5				10						15	
Ile	Gly	Ser	Phe	Lys	Gly	Val	Gly	Ala	Ile	Gly	Gly	Val	Gly	Ala	Val
			20					25					30		
Val	Phe	Gly	Ile	Ser	Leu	Phe	Ser	Phe	Gly	Gly	Phe	Cys	His	Asn	Ser
		35					40					45			
Val	Lys	Ala	Ala	Ala	Phe	Leu	Gly	Ser	Ile	Leu	Ala	Lys	Ile	Leu	Pro
	50					55					60				
Ser	Ser	Trp	Gly	Phe	Ser	Ala	Ile	Lys	Ile	Ser	Asn	Ala	Phe		
65					70					75					

<210> 121

<211> 1051

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(998)

<400> 121

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																	1	
tta	aat	act	ttc	ttg	gat	aca	tgt	ttt	ctt	tta	ttc	atc	agt	att	ctt			104
Leu	Asn	Thr	Phe	Leu	Asp	Thr	Cys	Phe	Leu	Leu	Phe	Ile	Ser	Ile	Leu			
			5				10					15						
ttt	tat	tta	agt	ata	cca	att	tat	cct	aac	aaa	gtg	gtg	gtt	gtc	ccg			152
Phe	Tyr	Leu	Ser	Ile	Pro	Ile	Tyr	Pro	Asn	Lys	Val	Val	Val	Val	Pro			
	20					25					30							
caa	ggt	tcg	ctc	aaa	aaa	gtg	ttt	ttt	tct	tta	aaa	gag	caa	ggc	gtg			200
Gln	Gly	Ser	Leu	Lys	Lys	Val	Phe	Phe	Ser	Leu	Lys	Glu	Gln	Gly	Val			
	35				40					45					50			
gat	atg	aac	gct	ttg	gat	ttg	ctt	ttt	tta	cgc	ctg	atg	ggc	atg	cct			248
Asp	Met	Asn	Ala	Leu	Asp	Leu	Leu	Phe	Leu	Arg	Leu	Met	Gly	Met	Pro			
				55					60					65				
aaa	aaa	ggt	tat	att	gat	atg	ggc	gat	ggg	gct	tta	agg	aag	ggg	gat			296
Lys	Lys	Gly	Tyr	Ile	Asp	Met	Gly	Asp	Gly	Ala	Leu	Arg	Lys	Gly	Asp			
			70					75					80					
ttt	tta	gtc	cgt	ttg	att	aag	gca	aaa	gcg	gca	caa	aaa	agt	gcg	act			344
Phe	Leu	Val	Arg	Leu	Ile	Lys	Ala	Lys	Ala	Ala	Gln	Lys	Ser	Ala	Thr			
		85					90					95						
cta	atc	cct	ggg	gaa	agc	cgc	tat	ttt	ttc	acg	caa	att	ttg	agc	gag			392
Leu	Ile	Pro	Gly	Glu	Ser	Arg	Tyr	Phe	Phe	Thr	Gln	Ile	Leu	Ser	Glu			

100	105	110	
act tac caa cta gaa aca agc gat ctc aat cag gct tat gaa agc atc			440
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile			
115	120	125	130
gct cca cga ttg aat ggc gaa gtg ata gaa gat ggg gtg ata tgg cca			488
Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile Trp Pro			
	135	140	145
gac act tat cat ttg cct tta ggg gag gac gct ttt aaa atc atg caa			536
Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln			
	150	155	160
act ttg att ggt caa tcc atg aaa aaa cac gaa gcc tta agc aaa caa			584
Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln			
	165	170	175
tgg ctt gga tac tac cat aaa gaa gag tgg ttt gaa aaa atc att ctc			632
Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu			
	180	185	190
gct tct att gtg caa aaa gaa gcc gct aat gtt gaa gaa atg ccc ttg			680
Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu			
195	200	205	210
att gcg agc gtg att ttt aac cgc ttg aaa aaa ggc atg cct tta caa			728
Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln			
	215	220	225
atg gat ggg gct ttg aat tat cag gaa ttt tca cac gct aaa gta acc			776
Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys Val Thr			
	230	235	240
aaa gag cgc att aaa acc gat aac acc ccc tac aat acc tat aaa ttt			824
Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr Lys Phe			
	245	250	255
aag ggt ttg cct aaa aat cct gta ggg agc gtg agc cta gaa gcg att			872
Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu Ala Ile			
	260	265	270
aga gcc gtg atc ttc cct aaa aaa acg gat ttc ttg tat ttt gtg aaa			920
Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe Val Lys			
275	280	285	290
atg ccg gat aaa aaa cat gct ttc agc gcg act tat aaa gag cat tta			968
Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu His Leu			
	295	300	305
aaa aac att aat ctt tct aat aat cat ttt taagattaag gtaaatgggg			1018
Lys Asn Ile Asn Leu Ser Asn Asn His Phe			
	310	315	
cgtttttttct tttgaattga gtaaaaagtg ttt			1051

<210> 122
 <211> 316
 <212> PRT
 <213> Helicobacter pylori

<400> 122
 Met Thr Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser
 1 5 10 15
 Ile Leu Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val
 20 25 30
 Val Pro Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln
 35 40 45
 Gly Val Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly
 50 55 60
 Met Pro Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys
 65 70 75 80
 Gly Asp Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser
 85 90 95
 Ala Thr Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu
 100 105 110
 Ser Glu Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu
 115 120 125
 Ser Ile Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile
 130 135 140
 Trp Pro Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile
 145 150 155 160
 Met Gln Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser
 165 170 175
 Lys Gln Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile
 180 185 190
 Ile Leu Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met
 195 200 205
 Pro Leu Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro
 210 215 220
 Leu Gln Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys
 225 230 235 240
 Val Thr Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr
 245 250 255
 Lys Phe Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu
 260 265 270
 Ala Ile Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe
 275 280 285
 Val Lys Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu
 290 295 300
 His Leu Lys Asn Ile Asn Leu Ser Asn Asn His Phe
 305 310 315

<210> 123
 <211> 637
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS

<222> (51)...(584)

<400> 123

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gaaagttcgg gggcggattc tatgattaat ggctatgggtt ataccaaaga atg agt      56
                                     Met Ser
                                     1

caa aaa atc cta att cta ggt att ggc aat atc ctt ttt ggc gat gaa      104
Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu
      5              10              15

ggg att ggg gtg cat tta gcc cac tac ctc aaa aaa aat ttt tct ttt      152
Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe
      20              25              30

ttc cct agc gtg gat att ata gat ggg ggg aca atg gcc cag cag ctc      200
Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu
      35              40              45

att cct tta atc act tcg tat gaa aag gtt ttg att ttg gat tgc gtg      248
Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val
      55              60              65

agc gct gaa ggc gtt gag ata gga tca gtc tat gct ttt gat ttt aag      296
Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys
      70              75              80

gac gct cct aaa gaa atc aca tgg gct ggg agc gct cat gaa gtg gaa      344
Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu
      85              90              95

atg cta cac act tta agg ctc acg gag ttt tta ggg gat ttg cct aaa      392
Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys
      100             105             110

act ttt atc gtg ggg ctt gtg cct ttt gtg ata ggg agc gag acc act      440
Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr
      115             120             125             130

ttc aag ctt tca agc aaa att tta aac gct tta gaa acc gcc tta aaa      488
Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys
      135             140             145

gcc ata gaa acc caa ctc aac gca tgg ggg gtt aaa atg caa cgc acc      536
Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr
      150             155             160

gat cat atc gct tta gaa tgt atc gct gaa ctt tct tat aag ggt ttt      584
Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe
      165             170             175

tgaattgggtt tttgtttttc tttttaaatg cgттаатgaa gaaacaagcc tga      637
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<210> 124

<211> 178

<212> PRT

<213> Helicobacter pylori

<400> 124

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Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly
 1           5           10           15
Asp Glu Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe
      20           25           30
Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln
      35           40           45
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp
      50           55           60
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp
65           70           75           80
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu
      85           90           95
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu
      100          105          110
Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu
      115          120          125
Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala
      130          135          140
Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln
145          150          155          160
Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys
      165          170          175
Gly Phe
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<210> 125

<211> 214

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(161)

<400> 125

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gcattgctaa tttgggaata cttgtttatg ccagtgaat aggagcggct atg atg      56
                                     Met Met
                                     1

tgg cgt agt ctc arg gtg gct ttt acg atc act gat att agt aaa acc      104
Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser Lys Thr
      5           10           15

ttt caa tcc cag cct aag cac cat caa atc ggc act tta gaa ttg aat      152
Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu Leu Asn
      20           25           30

ttc gcc ttt tgatttaata tcagtttaat atttttcttc ctatatgata      201
Phe Ala Phe
      35
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tttatatgat att

214

<210> 126

<211> 37

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 7

<223> Xaa = Any Amino Acid

<400> 126

Met	Met	Trp	Arg	Ser	Leu	Xaa	Val	Ala	Phe	Thr	Ile	Thr	Asp	Ile	Ser
1				5					10					15	
Lys	Thr	Phe	Gln	Ser	Gln	Pro	Lys	His	His	Gln	Ile	Gly	Thr	Leu	Glu
			20					25					30		
Leu	Asn	Phe	Ala	Phe											
			35												

<210> 127

<211> 1576

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1523)

<400> 127

ctgtattcgc	ttctgtggat	tactaccctc	aaagaaaaga	aagccacaga	atg aac	56
					Met Asn	
					1	
acc acc atc	tta gaa gct	tat gcg gct	gag cca agc	agg caa acc	ctc	104
Thr Thr Ile	Leu Glu Ala	Tyr Ala Ala	Glu Pro Ser	Arg Gln Thr	Leu	
	5		10		15	
tct aaa gtc	agc aac cga	ttc aaa gag	cat ggc gct	aaa ttt gat	ctt	152
Ser Lys Val	Ser Asn Arg	Phe Lys Glu	His Gly Ala	Lys Phe Asp	Leu	
	20		25		30	
cgt gtg atg	gca acg cat	gga ggc acc	att agt tgg	aaa gct aaa	gaa	200
Arg Val Met	Ala Thr His	Gly Gly Thr	Ile Ser Trp	Lys Ala Lys	Glu	
	35		40		45	50
ctc gct agg	act att gtg	agc ggc cct	att gga ggc	gtg att gga	tct	248
Leu Ala Arg	Thr Ile Val	Ser Gly Pro	Ile Gly Gly	Val Ile Gly	Ser	
	55		60		65	
aaa ttg cta	ggc gaa acg	ctt ggt tat	gac aat att	gca tgc agt	gat	296
Lys Leu Leu	Gly Glu Thr	Leu Gly Tyr	Asp Asn Ile	Ala Cys Ser	Asp	
	70		75		80	

att ggc ggc acg agc ttt gat atg gcg ctt atc gtt aag agc aat ttt	344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe	
85 90 95	
aac atc gct tct gac cct gat atg gca cgc ctt gtt tta tct cta ccg	392
Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser Leu Pro	
100 105 110	
ctt gtg gct atg gat tct gtt ggc gca ggt gct ggg agt ttt gtg cgc	440
Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe Val Arg	
115 120 125 130	
att gat cca cac agc cga tct gtc aaa cta ggg cct gac agc gcg ggg	488
Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser Ala Gly	
135 140 145	
tat aga gtt ggc act tgt tgg aaa gac agc ggg tta gac acg gtt tca	536
Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr Val Ser	
150 155 160	
gta acc gat tgc cat att gtt tta ggc tat ttg aac ccg gat aat ttc	584
Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp Asn Phe	
165 170 175	
tta ggc ggt ttg atc aaa tta gat gtg gat agg gct aaa aaa cac att	632
Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys His Ile	
180 185 190	
aaa gaa caa atc gct gat ccg cta ggc att agc gta gaa gat gcg gct	680
Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp Ala Ala	
195 200 205 210	
gct ggt gtg att gaa ttg ctt gat ttg gag ctt aaa gaa tac ttg cga	728
Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr Leu Arg	
215 220 225	
tcc aac att agc gct aaa ggg tat agc cca tct gat ttt gtg tgc ttt	776
Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val Cys Phe	
230 235 240	
tca tat ggt ggc gca gga cct gtg cat acc tat ggc tat aca gaa gga	824
Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr Glu Gly	
245 250 255	
tta ggg ttt aag gat gtg gta gtg cct gcg tgg gcg gct gga ttt agc	872
Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly Phe Ser	
260 265 270	
gct ttt ggt tgt gct tgc gct gat ttt gaa tac aga tac gac aag agc	920
Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp Lys Ser	
275 280 285 290	
gtg gat att gcc att ccg cag tat tct tca gac aag tca aaa ata gac	968
Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys Ile Asp	

295	300	305	
gca tgc aaa atc att caa gac gca tgg gat gaa ttg act ttg aaa gtg	1016		
Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu Lys Val			
310	315	320	
att gaa gag ttc aag atc aat gga ttt tct caa aaa gat gtg atc tta	1064		
Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val Ile Leu			
325	330	335	
aga cct gga tac agg atg cag tat atg ggg caa ttg aat gat tta gag	1112		
Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp Leu Glu			
340	345	350	
atc act tct cct gtg tca aaa gct gca agc gtg gct gat tgg gaa gag	1160		
Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp Glu Glu			
355	360	365	370
att gtc aaa gaa tat gaa aaa acc tac gct cgc gtt tat tct gaa tca	1208		
Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser Glu Ser			
375	380	385	
gcg tgt tct cca gag ctt ggt ttt agc gtg act ggc gtg atc atg cgt	1256		
Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg			
390	395	400	
ggt gtt gtg gct acg caa aaa cct gtg att ccg gtt gaa aaa gag cat	1304		
Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His			
405	410	415	
ggt gct acg ccc cca aaa gaa gcc aaa ata ggc gtt aga aaa ttc tat	1352		
Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr			
420	425	430	
cgg cat aaa aaa tgg gtg gat gca gat gtg tgg caa atg gaa aaa tta	1400		
Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu			
435	440	445	450
ctg cct gga aat gaa gtc ata gga cct gcg atc gtg gaa tca gat gcg	1448		
Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala			
455	460	465	
acc act ttc gtg ata ccc aaa ggc ttt gcg aca aga cta gac aaa cac	1496		
Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His			
470	475	480	
cga ttg ttc cac ttg aaa gaa att aaa taaaggagtt caaaatggca	1543		
Arg Leu Phe His Leu Lys Glu Ile Lys			
485	490		
aattttattga aaaacggcaa aacttttaaaa caa	1576		
<210> 128			
<211> 491			
<212> PRT			

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 84

<223> Xaa = Any Amino Acid

<400> 128

Met	Asn	Thr	Thr	Ile	Leu	Glu	Ala	Tyr	Ala	Ala	Glu	Pro	Ser	Arg	Gln
1				5					10					15	
Thr	Leu	Ser	Lys	Val	Ser	Asn	Arg	Phe	Lys	Glu	His	Gly	Ala	Lys	Phe
			20					25					30		
Asp	Leu	Arg	Val	Met	Ala	Thr	His	Gly	Gly	Thr	Ile	Ser	Trp	Lys	Ala
			35				40					45			
Lys	Glu	Leu	Ala	Arg	Thr	Ile	Val	Ser	Gly	Pro	Ile	Gly	Gly	Val	Ile
	50					55					60				
Gly	Ser	Lys	Leu	Leu	Gly	Glu	Thr	Leu	Gly	Tyr	Asp	Asn	Ile	Ala	Cys
65					70					75					80
Ser	Asp	Ile	Xaa	Gly	Thr	Ser	Phe	Asp	Met	Ala	Leu	Ile	Val	Lys	Ser
			85					90						95	
Asn	Phe	Asn	Ile	Ala	Ser	Asp	Pro	Asp	Met	Ala	Arg	Leu	Val	Leu	Ser
			100					105					110		
Leu	Pro	Leu	Val	Ala	Met	Asp	Ser	Val	Gly	Ala	Gly	Ala	Gly	Ser	Phe
			115				120					125			
Val	Arg	Ile	Asp	Pro	His	Ser	Arg	Ser	Val	Lys	Leu	Gly	Pro	Asp	Ser
	130					135					140				
Ala	Gly	Tyr	Arg	Val	Gly	Thr	Cys	Trp	Lys	Asp	Ser	Gly	Leu	Asp	Thr
145					150					155					160
Val	Ser	Val	Thr	Asp	Cys	His	Ile	Val	Leu	Gly	Tyr	Leu	Asn	Pro	Asp
			165					170						175	
Asn	Phe	Leu	Gly	Leu	Ile	Lys	Leu	Asp	Val	Asp	Arg	Ala	Lys	Lys	
			180				185					190			
His	Ile	Lys	Glu	Gln	Ile	Ala	Asp	Pro	Leu	Gly	Ile	Ser	Val	Glu	Asp
		195					200					205			
Ala	Ala	Ala	Gly	Val	Ile	Glu	Leu	Leu	Asp	Leu	Glu	Leu	Lys	Glu	Tyr
	210					215				220					
Leu	Arg	Ser	Asn	Ile	Ser	Ala	Lys	Gly	Tyr	Ser	Pro	Ser	Asp	Phe	Val
225				230						235					240
Cys	Phe	Ser	Tyr	Gly	Gly	Ala	Gly	Pro	Val	His	Thr	Tyr	Gly	Tyr	Thr
			245						250					255	
Glu	Gly	Leu	Gly	Phe	Lys	Asp	Val	Val	Val	Pro	Ala	Trp	Ala	Ala	Gly
			260				265					270			
Phe	Ser	Ala	Phe	Gly	Cys	Ala	Cys	Ala	Asp	Phe	Glu	Tyr	Arg	Tyr	Asp
		275				280						285			
Lys	Ser	Val	Asp	Ile	Ala	Ile	Pro	Gln	Tyr	Ser	Ser	Asp	Lys	Ser	Lys
	290					295					300				
Ile	Asp	Ala	Cys	Lys	Ile	Ile	Gln	Asp	Ala	Trp	Asp	Glu	Leu	Thr	Leu
305				310						315					320
Lys	Val	Ile	Glu	Glu	Phe	Lys	Ile	Asn	Gly	Phe	Ser	Gln	Lys	Asp	Val
			325						330					335	
Ile	Leu	Arg	Pro	Gly	Tyr	Arg	Met	Gln	Tyr	Met	Gly	Gln	Leu	Asn	Asp
			340				345						350		
Leu	Glu	Ile	Thr	Ser	Pro	Val	Ser	Lys	Ala	Ala	Ser	Val	Ala	Asp	Trp
		355				360						365			
Glu	Glu	Ile	Val	Lys	Glu	Tyr	Glu	Lys	Thr	Tyr	Ala	Arg	Val	Tyr	Ser

370		375		380
Glu Ser Ala Cys Ser Pro	Glu Leu Gly Phe Ser Val Thr Gly Val Ile			
385		390	395	400
Met Arg Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys				
		405	410	415
Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys				
		420	425	430
Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu				
		435	440	445
Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser				
		450	455	460
Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp				
465		470	475	480
Lys His Arg Leu Phe His Leu Lys Glu Ile Lys				
		485	490	

<210> 129
 <211> 303
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(261)

<400> 129
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 Met Ile
 1

cag tta aaa tca aat ttg gat tgg tac gca gat tat ttg aat ttt tta 105
 Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn Phe Leu
 5 10 15

gat cgc ttt ggg gaa aaa atg gaa gaa tcc aaa gag cga aaa caa ctc 153
 Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys Gln Leu
 20 25 30

ctg atc gct tcc ctt gca cct ctt gcg ggc ttt gct gca aga ata tcg 201
 Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg Ile Ser
 35 40 45 50

ccg gga tta ttg agc tta ttg ggt ttg atg ctg gca atg ggg tgt gca 249
 Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly Cys Ala
 55 60 65

aat ttt tgg att tagaaaccaa tctgtgcaag atttatgaat cgcgcccgtt 301
 Asn Phe Trp Ile
 70

aa 303

<210> 130
 <211> 70

<212> PRT

<213> Helicobacter pylori

<400> 130

Met	Ile	Gln	Leu	Lys	Ser	Asn	Leu	Asp	Trp	Tyr	Ala	Asp	Tyr	Leu	Asn
1				5				10						15	
Phe	Leu	Asp	Arg	Phe	Gly	Glu	Lys	Met	Glu	Glu	Ser	Lys	Glu	Arg	Lys
			20					25					30		
Gln	Leu	Leu	Ile	Ala	Ser	Leu	Ala	Pro	Leu	Ala	Gly	Phe	Ala	Ala	Arg
		35					40					45			
Ile	Ser	Pro	Gly	Leu	Leu	Ser	Leu	Leu	Gly	Leu	Met	Leu	Ala	Met	Gly
	50					55					60				
Cys	Ala	Asn	Phe	Trp	Ile										
65					70										

<210> 131

<211> 826

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(773)

<400> 131

tggttaatt	gttaagccgg	ctagaaaaag	agcggttattt	gcgccatattc	atg	cta	56
					Met	Leu	
					1		
gaa	gat	gtg	ggc	gaa	gag	ggg	104
Glu	Asp	Val	Gly	Glu	Glu	Gly	
		5				10	
						15	
tta	gtc	att	ggg	gct	ggg	ggg	152
Leu	Val	Ile	Gly	Ala	Gly	Gly	
		20				25	
						30	
tgt	gcc	gct	ggg	ata	gga	aaa	200
Cys	Ala	Ala	Gly	Ile	Gly	Lys	
		35				40	
						45	
						50	
gat	atg	agt	aat	ttg	caa	cgc	248
Asp	Met	Ser	Asn	Leu	Gln	Arg	
			55			60	
						65	
aac	caa	tct	aaa	gcc	tct	agc	296
Asn	Gln	Ser	Lys	Ala	Ser	Ser	
		70				75	
						80	
gcg	ggg	att	gaa	ata	gag	gct	344
Ala	Gly	Ile	Glu	Ile	Glu	Ala	
		85				90	
						95	
gct	ctt	tct	ctc	ata	gag	cct	392
						tat	
						gat	
						ttt	
						atc	
						ata	
						gac	
						gcc	
						acg	
						gac	

Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala Thr Asp
100 105 110

aat ttt aac gct aaa ttt ttg atc aat gac gct tgc gtg tta gcc caa 440
Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu Ala Gln
115 120 125 130

aaa ccc tat tcg cat gcc ggg gtt tta gaa tac agg ggg caa agc atg 488
Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln Ser Met
135 140 145

agc gtt tta ccc cat agc gca tgc tta gcg tgc gtt ttt gat aag ccc 536
Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp Lys Pro
150 155 160

cct aaa aag gga tta aat ccc att tca ggg ctt ttt ggg gtc tta ccc 584
Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val Leu Pro
165 170 175

gga gtt tta ggg tgt atc caa gcg agc gaa tgc ctt aaa tat ttt tta 632
Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr Phe Leu
180 185 190

ggg ttt gaa act tta ctt ata aat act tta ctt ata gcc gat att aaa 680
Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp Ile Lys
195 200 205 210

acg atg gat ttt aaa aaa att caa gca ccc aaa aac cct gaa tgt agg 728
Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu Cys Arg
215 220 225

gtt tgt ggc acg cat aaa atc acg cat tta cag gat tat gaa att 773
Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu Ile
230 235 240

tagattaagg ggtaagtttt ggatttatca accatattag gcttggtatt ggc 826

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<212> PRT
<213> Helicobacter pylori

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Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met
20 25 30
Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp
35 40 45
Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp
50 55 60
Phe Leu Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln
65 70 75 80
Leu Asn Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala
85 90 95

His	Asn	Ala	Leu	Ser	Leu	Ile	Glu	Pro	Tyr	Asp	Phe	Ile	Ile	Asp	Ala
			100					105					110		
Thr	Asp	Asn	Phe	Asn	Ala	Lys	Phe	Leu	Ile	Asn	Asp	Ala	Cys	Val	Leu
		115					120					125			
Ala	Gln	Lys	Pro	Tyr	Ser	His	Ala	Gly	Val	Leu	Glu	Tyr	Arg	Gly	Gln
	130					135					140				
Ser	Met	Ser	Val	Leu	Pro	His	Ser	Ala	Cys	Leu	Ala	Cys	Val	Phe	Asp
145					150					155					160
Lys	Pro	Pro	Lys	Lys	Gly	Leu	Asn	Pro	Ile	Ser	Gly	Leu	Phe	Gly	Val
			165					170						175	
Leu	Pro	Gly	Val	Leu	Gly	Cys	Ile	Gln	Ala	Ser	Glu	Cys	Leu	Lys	Tyr
		180						185					190		
Phe	Leu	Gly	Phe	Glu	Thr	Leu	Leu	Ile	Asn	Thr	Leu	Leu	Ile	Ala	Asp
	195					200					205				
Ile	Lys	Thr	Met	Asp	Phe	Lys	Lys	Ile	Gln	Ala	Pro	Lys	Asn	Pro	Glu
	210					215					220				
Cys	Arg	Val	Cys	Gly	Thr	His	Lys	Ile	Thr	His	Leu	Gln	Asp	Tyr	Glu
225					230					235					240
Ile															

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 <213> *Helicobacter pylori*

<220>
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<400> 133																	
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														1			
cgc atg aat aaa aat tat ctt tta atc ttt ttg ttg tta gcg agt ctt															104		
Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu																	
														5	10	15	
ggt gct aga gag aag gac gct tct tca aac ctt ttt gat ttg att gat															152		
Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp																	
														20	25	30	
aag ggg atc aac aga gaa caa gaa tta aaa gag cag gag caa aaa acg															200		
Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln Lys Thr																	
														35	40	45	50
cgc tta aaa ctg gct caa agc cct tta gta gcg tta gag att gtc ccc															248		
Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile Val Pro																	
														55	60	65	
caa gaa acg ccc tat tta gaa tgg caa ggg gct agg gag tcg tat tat															296		
Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser Tyr Tyr																	
														70	75	80	

tta aag gtg agc gct gta gtg gag agc gtg gtt atc tta aaa att gac	344
Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp	
85 90 95	

atc aat caa ggg cgt tct tgc tgc ctc tac ccc acg cct aaa agc gtt	392
Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val	
100 105 110	

tct tta gtg agg aat caa agc gta gcc tat gaa att tta tgc gaa aac	440
Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn	
115 120 125 130	

caa ccc cta tgg ata gaa gta agc acc aat tta ggc aaa cgc acc ttt	488
Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg Thr Phe	
135 140 145	

cag ttt taacctgcaa ccaacattaa agaatgcctt tagcatttta aaaccccttt	544
Gln Phe	

atc	547
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 <213> Helicobacter pylori

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20 25 30	
Ile Asp Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln	
35 40 45	
Lys Thr Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile	
50 55 60	
Val Pro Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser	
65 70 75 80	
Tyr Tyr Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys	
85 90 95	
Ile Asp Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys	
100 105 110	
Ser Val Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys	
115 120 125	
Glu Asn Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg	
130 135 140	
Thr Phe Gln Phe	
145	

<210> 135
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 <212> DNA
 <213> Helicobacter pylori

<220>

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<222> (51)...(1631)

<400> 135

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                                     Met Leu
                                     1

gct tcc atc atc tca att tta agg gtt ttt gtt ttg tta ttc aac acg      104
Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr
      5                      10                      15

ccg tta ttc atc ttt gct ttt ttg cct gtt ggt ttt tta ggg tat ttt      152
Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe
      20                      25                      30

atc ttg caa gct tat gct aaa aat ccc ctg ttc cct aaa cta tgg cta      200
Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu
      35                      40                      45                      50

gta ttg gct agt ttg ttt ttt tat gct ttt tgg aat gtg aag tat ttg      248
Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu
      55                      60                      65

ccc tta ttg gtt ggc tct att gtt ttt aat tat ttt gtg gct ttg aaa      296
Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys
      70                      75                      80

atc cat caa acc cag cca aat gca tat aaa aga tta tgg ctt att ttg      344
Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu
      85                      90                      95

ggc ttg atc gct aat gtt tca ctt tta gga ttt ttc aaa tac act gat      392
Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp
      100                      105                      110

ttt ttc tta acc aat ttc aat cta ata tgg aag agc cat ttt gaa acc      440
Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe Glu Thr
      115                      120                      125                      130

ttg cat tta atc ttg cct tta gcg atc agc ttt ttc act ttg caa caa      488
Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu Gln Gln
      135                      140                      145

atc gct tac ttg atg gac act tat aag caa aat caa atc atg cag ccc      536
Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met Gln Pro
      150                      155                      160

aaa atg aga gag aga gtg agt gaa aac gct cct att tta tta aat cct      584
Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu Asn Pro
      165                      170                      175

ccc act tca ttt ttt tca ctt tcg cat ttt tta gat tac gct tta ttt      632
Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala Leu Phe
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180	185	190	
gtg agt ttc ttc cct caa ctc att gca ggg cct att gtg cat cat agc			680
Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His His Ser			
195	200	205	210
gag atg atg cct caa ttt aaa gat aaa aac aat caa tat ttg aat tac			728
Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu Asn Tyr			
	215	220	225
aga aat atc gct tta ggc ttg ttt atc ttt tct atc ggt ttg ttt aaa			776
Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu Phe Lys			
	230	235	240
aag gtc gtg att gca gat aat acc gct cat ttt gct gat ttt gga ttt			824
Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe Gly Phe			
	245	250	255
gat aag gcg act agc tta agt ttt att caa gca tgg atg act tct tta			872
Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr Ser Leu			
	260	265	270
tct tat tcg ttc cag ctg tat ttt gat ttt agc ggt tat tgc gat atg			920
Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys Asp Met			
275	280	285	290
gct ata ggc att ggc ctc ttt ttt aac atc aaa ctc cct atc aat ttt			968
Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile Asn Phe			
	295	300	305
aat agc ccc tat aag gct ttg aat atc caa gat ttt tgg agg agg tgg			1016
Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg Arg Trp			
	310	315	320
cat atc act ttg agc cgc ttc tta aaa gag tat ttg tat atc cct tta			1064
His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile Pro Leu			
	325	330	335
ggg ggt aat agg gtg aaa gaa tta atc gtg tat agg aat tta att tta			1112
Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu Ile Leu			
	340	345	350
gtg ttt ttg att ggg ggg ttt tgg cat ggg gct ggt tgg act ttt atc			1160
Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile			
355	360	365	370
att tgg ggg cta ttg cat ggg att gct ttg agc gtt cat aga gcg tat			1208
Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr			
	375	380	385
tct cat gcc act aga aaa ttc cat ttc act atg cca aag att tta gca			1256
Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala			
	390	395	400
tgg ctc atc act ttt aat ttt atc aat ctc gca tgg gtg ttt ttt aga			1304

Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe Phe Arg
 405 410 415
 gcc aaa aat tta gaa agc gct ttg aag gtt tta aag ggg atg gtt ggt 1352
 Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met Val Gly
 420 425 430
 ttg aat ggt gtt tcg ctt tgt cat ctt tca aaa gag gca tca gag ttt 1400
 Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser Glu Phe
 435 440 445 450
 tta aat cgt gtc aat gat aac atg atc atg cac acc ata atg tat gca 1448
 Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met Tyr Ala
 455 460 465
 tcc ccc aca ttt aaa atg tgt gtt ttg atg ata atc atc tct ttt tgt 1496
 Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser Phe Cys
 470 475 480
 tta aaa aat agt tcc cat tta tac caa tcc aat caa atg gat tgg att 1544
 Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp Trp Ile
 485 490 495
 aaa aca aca agc gct tgt ttg ttg ctc tct ata ggt ttt tta ttt att 1592
 Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu Phe Ile
 500 505 510
 ttt gcc agt tct caa tcg gta ttt ttg tat ttt aat ttt taggacactg 1641
 Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
 515 520 525
 ctatggaatt ttataaaaaa caaactttaa tcattgtttc ttt 1684
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 <213> *Helicobacter pylori*
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 Asn Thr Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly
 20 25 30
 Tyr Phe Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu
 35 40 45
 Trp Leu Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys
 50 55 60
 Tyr Leu Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala
 65 70 75 80
 Leu Lys Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu
 85 90 95
 Ile Leu Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr
 100 105 110
 Thr Asp Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe
 115 120 125

Glu	Thr	Leu	His	Leu	Ile	Leu	Pro	Leu	Ala	Ile	Ser	Phe	Phe	Thr	Leu
130						135					140				
Gln	Gln	Ile	Ala	Tyr	Leu	Met	Asp	Thr	Tyr	Lys	Gln	Asn	Gln	Ile	Met
145					150					155					160
Gln	Pro	Lys	Met	Arg	Glu	Arg	Val	Ser	Glu	Asn	Ala	Pro	Ile	Leu	Leu
			165						170					175	
Asn	Pro	Pro	Thr	Ser	Phe	Phe	Ser	Leu	Ser	His	Phe	Leu	Asp	Tyr	Ala
			180					185					190		
Leu	Phe	Val	Ser	Phe	Phe	Pro	Gln	Leu	Ile	Ala	Gly	Pro	Ile	Val	His
	195						200					205			
His	Ser	Glu	Met	Met	Pro	Gln	Phe	Lys	Asp	Lys	Asn	Asn	Gln	Tyr	Leu
210						215					220				
Asn	Tyr	Arg	Asn	Ile	Ala	Leu	Gly	Leu	Phe	Ile	Phe	Ser	Ile	Gly	Leu
225				230					235						240
Phe	Lys	Lys	Val	Val	Ile	Ala	Asp	Asn	Thr	Ala	His	Phe	Ala	Asp	Phe
			245						250					255	
Gly	Phe	Asp	Lys	Ala	Thr	Ser	Leu	Ser	Phe	Ile	Gln	Ala	Trp	Met	Thr
			260					265					270		
Ser	Leu	Ser	Tyr	Ser	Phe	Gln	Leu	Tyr	Phe	Asp	Phe	Ser	Gly	Tyr	Cys
	275						280					285			
Asp	Met	Ala	Ile	Gly	Ile	Gly	Leu	Phe	Phe	Asn	Ile	Lys	Leu	Pro	Ile
290						295					300				
Asn	Phe	Asn	Ser	Pro	Tyr	Lys	Ala	Leu	Asn	Ile	Gln	Asp	Phe	Trp	Arg
305					310					315					320
Arg	Trp	His	Ile	Thr	Leu	Ser	Arg	Phe	Leu	Lys	Glu	Tyr	Leu	Tyr	Ile
			325						330					335	
Pro	Leu	Gly	Gly	Asn	Arg	Val	Lys	Glu	Leu	Ile	Val	Tyr	Arg	Asn	Leu
		340						345					350		
Ile	Leu	Val	Phe	Leu	Ile	Gly	Gly	Phe	Trp	His	Gly	Ala	Gly	Trp	Thr
	355					360						365			
Phe	Ile	Ile	Trp	Gly	Leu	Leu	His	Gly	Ile	Ala	Leu	Ser	Val	His	Arg
370					375						380				
Ala	Tyr	Ser	His	Ala	Thr	Arg	Lys	Phe	His	Phe	Thr	Met	Pro	Lys	Ile
385					390					395					400
Leu	Ala	Trp	Leu	Ile	Thr	Phe	Asn	Phe	Ile	Asn	Leu	Ala	Trp	Val	Phe
			405						410					415	
Phe	Arg	Ala	Lys	Asn	Leu	Glu	Ser	Ala	Leu	Lys	Val	Leu	Lys	Gly	Met
			420					425					430		
Val	Gly	Leu	Asn	Gly	Val	Ser	Leu	Cys	His	Leu	Ser	Lys	Glu	Ala	Ser
		435					440					445			
Glu	Phe	Leu	Asn	Arg	Val	Asn	Asp	Asn	Met	Ile	Met	His	Thr	Ile	Met
450						455					460				
Tyr	Ala	Ser	Pro	Thr	Phe	Lys	Met	Cys	Val	Leu	Met	Ile	Ile	Ile	Ser
465					470					475					480
Phe	Cys	Leu	Lys	Asn	Ser	Ser	His	Leu	Tyr	Gln	Ser	Asn	Gln	Met	Asp
			485						490					495	
Trp	Ile	Lys	Thr	Ser	Ala	Cys	Leu	Leu	Leu	Ser	Ile	Gly	Phe	Leu	
		500					505					510			
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<213> Helicobacter pylori

<220>

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<400> 137

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Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala
      5                      10                      15

tta gta gga gcg tta gtc agc atc aca ccg caa caa agt cat gcc gcc      152
Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His Ala Ala
      20                      25                      30

ttt ttc aca acc gtg atc att cca gcc att gtt ggg ggg att gct aca      200
Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr
      35                      40                      45                      50

ggc gct gct gta gga acg gtc tca ggg ctt ctt ggc tgg ggg cta aaa      248
Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys
      55                      60                      65

caa gcc gaa gaa gcc aat aaa acc cca gat aaa ccc gat aaa gtt tgg      296
Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp
      70                      75                      80

cgc att caa gca gga aaa ggc ttt aat gaa ttc cct aac aag gaa tac      344
Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr
      85                      90                      95

gac tta tac aga tcc cta cta tct agt aag att gat gga ggc tgg gat      392
Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly Trp Asp
      100                      105                      110

tgg ggg aat gcc gct acg cat tat tgg gtc aaa ggc ggg caa tgg aac      440
Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln Trp Asn
      115                      120                      125                      130

aag ctt gaa gtg gat atg aaa gac gct gta ggg act tat aat ctc tca      488
Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn Leu Ser
      135                      140                      145

ggg cta aga aac ttt act ggt ggg gat tta gat gtc aat atg caa aaa      536
Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met Gln Lys
      150                      155                      160

gcc act ttg cgc ttg ggc caa ttc aat ggc aat tct ttc aca agc tat      584
Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr
      165                      170                      175
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aag gat agc gct gat cgc acc acg aga gtg gat ttc aac gct aaa aat	632
Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn	
180 185 190	
atc tta att gat aat ttt tta gaa atc aat aat cgt gtg ggt tct gga	680
Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly	
195 200 205 210	
gcc ggg agg aaa gcc agc tct acg gtt tta act ttg caa gct tca gaa	728
Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu	
215 220 225	
ggg att act agc agt aaa aat gcg gaa att tct ctt tat gat ggc gcc	776
Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala	
230 235 240	
acg ctc aat ttg gct tca aac agc gtt aaa tta atg ggt aat gtg tgg	824
Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp	
245 250 255	
atg ggc cgt ttg caa tat gtg gga gcg tat ttg gcc cct tca tac agc	872
Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser	
260 265 270	
acg ata aac act tca aaa gtg aca ggg gaa gtg aat ttt aac cat ctc	920
Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu	
275 280 285 290	
act gtg ggc gat cac aac gcc gct caa gca ggc att atc gct agt aac	968
Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn	
295 300 305	
aag act cat att ggc aca ctg gat ttg tgg caa agc gcg gga cta aac	1016
Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn	
310 315 320	
att atc gcc cct cca gaa ggc ggt tat aag gat aaa cct aag gat aaa	1064
Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys	
325 330 335	
cct agt aac acc acg caa aat aat gct aac aac aac caa caa aac agc	1112
Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser	
340 345 350	
gct caa aac aat agt aac act cag gtt att aac cca ccc aat agc gcg	1160
Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala	
355 360 365 370	
caa aaa aca gaa att caa ccc acg caa gtc att gat ggg cct ttt gct	1208
Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala	
375 380 385	
ggg ggc aaa gac acg gtt gtc aat att gat cgc atc aac act aac gct	1256
Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala	
390 395 400	

gat ggc acg att aaa gtg gga ggg tat aaa gct tct ctt acc acc aat	1304
Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn	
405 410 415	
gcg gct cat ttg cat atc ggc aaa ggc ggt atc aat ctg tcc aat caa	1352
Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln	
420 425 430	
gcg agc ggg cgc acc ctt tta gtg gaa aat cta acc ggg aat atc acc	1400
Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr	
435 440 445 450	
gtt gat ggg cct tta aga gtg aat aat caa gtg ggt ggt tat gct ttg	1448
Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu	
455 460 465	
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Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys	
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Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr	
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cct tat ttg ggc tat gac aaa cgc tat aaa aac tta atc cat gcg aca 1161
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr
355 360 365

ggg cta ggg tgg ctt ggc atc act ttt ggc cca gcc att ggt aaa atc 1209
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile
370 375 380 385

atc gcc aat ttg agc caa gac gga gcg aat gaa aaa aat gcc gat att 1257
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile
390 395 400

atg ctt ttt tct gca ttt ttt agg gat taaggaattt cttttttaaa 1304
Met Leu Phe Ser Ala Phe Phe Arg Asp
405 410

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<213> Helicobacter pylori

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35 40 45
Ser Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp
50 55 60
Thr Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe
65 70 75 80
Gly Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser
85 90 95
Ala Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr
100 105 110
Gly Trp Leu Ser Ile Asp Met Tyr His Gln Met Leu Lys Asp Gly Met
115 120 125
Asp Phe Trp Tyr Lys Glu Asp Gly Leu Leu Met Ile Tyr Thr Leu Glu
130 135 140
Glu Ser Phe Glu Lys Lys Leu Lys Thr Cys Asp Asn Ser Gly Ala Tyr
145 150 155 160
Lys Ile Leu Ser Ala Lys Glu Thr Lys Glu Tyr Met Pro Val Val Asn
165 170 175
Asp Asn Ile Cys Gly Ser Val Leu Leu Thr Glu Asn Ala His Val Asp
180 185 190
Pro Gly Glu Val Met His Ser Leu Gln Glu Tyr Leu Gln Asn Val Gly
195 200 205
Val Glu Phe Leu Tyr Asn Glu Glu Val Ile Asp Phe Glu Phe Lys Asn

210	215	220
Asn Leu Ile Glu Gly Val	Ile Thr His Lys Glu	Lys Ile Gln Ala Glu
225	230	235
Thr Ile Ile Leu Ala Thr	Gly Ala Asn Pro Thr	Leu Ile Lys Lys Thr
	245	250
Lys Asn Asp Phe Leu Met	Met Gly Ala Lys Gly	Tyr Ser Ile Thr Phe
	260	265
Lys Met Pro Glu Glu Leu	Lys Pro Lys Thr Ser	Ser Leu Phe Ala Asp
	275	280
Ile Phe Met Ala Met Thr	Pro Arg Arg Asp Thr	Val Arg Ile Thr Ser
	290	295
Lys Leu Glu Leu Asn Thr	Asn Asn Ala Leu Ile	Asp Lys Glu Gln Ile
305	310	315
Ala Asn Met Lys Lys Asn	Leu Ala Ala Phe Thr	Gln Pro Phe Glu Met
	325	330
Lys Asp Ala Ile Glu Trp	Cys Gly Phe Arg Pro	Leu Thr Pro Asn Asp
	340	345
Ile Pro Tyr Leu Gly Tyr	Asp Lys Arg Tyr Lys	Asn Leu Ile His Ala
	355	360
Thr Gly Leu Gly Trp Leu	Gly Ile Thr Phe Gly	Pro Ala Ile Gly Lys
	370	375
Ile Ile Ala Asn Leu Ser	Gln Asp Gly Ala Asn	Glu Lys Asn Ala Asp
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<220>
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cat aaa gaa atc gtt ata ggg gtt gat cta ggc tct aga aag att tgc	104
His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys Ile Cys	
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gcg ata gtg gct gaa ttt aaa gaa ggg att ttg cgc atc att ggc acg	152
Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile Gly Thr	
	20 25 30
gcc cat caa gac tcc aaa gaa atc aat tca aaa gcc att aaa aga ggg	200
Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys Arg Gly	
	35 40 45 50
cgt atc aat agc ctt gct cac gct tcc aac gcc att aaa gaa gtg att	248
Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu Val Ile	

55										60										65										
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			70					75						80																
aac	ccc	atg	ccc	cat	ttt	ggg	gaa	tac	cac	cct	aaa	act	aag	gcg	att	344														
Asn	Pro	Met	Pro	His	Phe	Gly	Glu	Tyr	His	Pro	Lys	Thr	Lys	Ala	Ile															
		85					90					95																		
gtt	tct	ttt	tct	ggg	gct	tat	act	gaa	agc	att	aga	gat	gtt	acc	ggc	392														
Val	Ser	Phe	Ser	Gly	Ala	Tyr	Thr	Glu	Ser	Ile	Arg	Asp	Val	Thr	Gly															
	100					105					110																			
gta	gcg	agc	acc	aaa	gat	aat	gtg	gta	acc	att	gat	gaa	atc	aat	cgc	440														
Val	Ala	Ser	Thr	Lys	Asp	Asn	Val	Val	Thr	Ile	Asp	Glu	Ile	Asn	Arg															
115					120					125					130															
gct	atc	aat	agt	gca	tgc	gct	aaa	gca	ggc	tta	gat	aac	gac	aaa	cat	488														
Ala	Ile	Asn	Ser	Ala	Cys	Ala	Lys	Ala	Gly	Leu	Asp	Asn	Asp	Lys	His															
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att	ttg	cat	gct	ctc	ccc	tat	cgc	ttc	act	tta	gac	aaa	caa	gaa	gtg	536														
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aat	gac	cct	tta	ggg	atg	agc	ggg	act	cgc	ttg	gaa	gtc	ttt	atc	cac	584														
Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe	Ile	His															
		165					170					175																		
att	gtc	tat	aca	gaa	aaa	aac	aac	att	gaa	aat	tta	gaa	aaa	atc	atg	632														
Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys	Ile	Met															
	180					185					190																			
atc	caa	tct	ggg	gta	gag	att	gaa	aac	atc	gtg	atc	aat	tct	tat	gca	680														
Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser	Tyr	Ala															
195					200					205					210															
gcc	tcg	att	gcc	acc	tta	tct	aat	gat	gaa	agg	gaa	ttg	ggc	gtg	gct	728														
Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly	Val	Ala															
				215					220					225																
tgc	gtg	gat	atg	ggc	gga	gag	aca	tgc	aac	ctt	acg	att	tat	agc	ggc	776														
Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr	Ser	Gly															
			230					235					240																	
aat	tcc	ata	cgc	tat	aac	aaa	tat	ttg	ccc	gta	ggc	tct	cac	cat	tta	824														
Asn	Ser	Ile	Arg	Tyr	Asn	Lys	Tyr	Leu	Pro	Val	Gly	Ser	His	His	Leu															
		245					250					255																		
acc	acg	gat	tta	tcg	cac	atg	ctc	aac	acc	cca	ttc	cct	tac	gct	gaa	872														
Thr	Thr	Asp	Leu	Ser	His	Met	Leu	Asn	Thr	Pro	Phe	Pro	Tyr	Ala	Glu															
	260					265					270																			
gaa	gtt	aag	atc	aaa	tac	ggg	gat	ctt	tct	ttt	gaa	ggc	ggc	gaa	gaa	920														

Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu	
275 280 285 290	
acg ccc tct caa aat gtc caa atc cct acc acc ggc tcg gat ggc cat	968
Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp Gly His	
295 300 305	
gaa agc cat att gtg ccg ctt agt gaa atc caa act atc atg aga gaa	1016
Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu	
310 315 320	
agg gct tta gaa act ttt aaa atc atc cac agg agc att caa gat agc	1064
Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser	
325 330 335	
ggc tta gaa gag cat ttg ggc gga ggc gtt gtg tta acc ggt ggg atg	1112
Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met	
340 345 350	
gct tta atg aaa ggg atc aaa gaa tta gcc aga acc cat ttc act aat	1160
Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn	
355 360 365 370	
tac ccg gtg cgt ttg gca gcc cct gtg gaa aaa tac aat atc atg ggc	1208
Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly	
375 380 385	
atg ttt gaa gat ttg aaa gac cct cgc ttt tca gtc gta gtt ggc ttg	1256
Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val Gly Leu	
390 395 400	
att tta tac aaa gca ggg ggg cat acc aat tat gaa aga gac tct aaa	1304
Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys	
405 410 415	
ggg gtt atc cgc tac cat gaa agc gat gat tac aca aga aca gcc cat	1352
Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His	
420 425 430	
caa tca agc cct acc ccc cat atc cat tca tcg ccc aca gaa agg aat	1400
Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn	
435 440 445 450	
ttg agc gat tta aaa gcc cct agt gct cct tta aac acc gct aaa aac	1448
Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn	
455 460 465	
gat gac ttt tta cct ata aaa ccc acc gaa caa aaa ggt ttt ttt aaa	1496
Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys	
470 475 480	
agt ttc ctt gat aag att tct aaa ttc ttt taagatacag ccatttcttt	1546
Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe	
485 490	

atgcgataaa aacgccttga tggttatcaa aag

1579

<210> 142

<211> 492

<212> PRT

<213> Helicobacter pylori

<400> 142

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Ile	Cys	Ala	Ile	Val	Ala	Glu	Phe	Lys	Glu	Gly	Ile	Leu	Arg	Ile	Ile
		20					25					30			
Gly	Thr	Ala	His	Gln	Asp	Ser	Lys	Glu	Ile	Asn	Ser	Lys	Ala	Ile	Lys
	35					40					45				
Arg	Gly	Arg	Ile	Asn	Ser	Leu	Ala	His	Ala	Ser	Asn	Ala	Ile	Lys	Glu
	50				55					60					
Val	Ile	Asn	Ser	Ala	Lys	Lys	Met	Ala	Gly	Leu	Asn	Ala	Asp	Glu	Asp
65				70					75					80	
Arg	Asn	Asn	Pro	Met	Pro	His	Phe	Gly	Glu	Tyr	His	Pro	Lys	Thr	Lys
		85						90					95		
Ala	Ile	Val	Ser	Phe	Ser	Gly	Ala	Tyr	Thr	Glu	Ser	Ile	Arg	Asp	Val
		100					105						110		
Thr	Gly	Val	Ala	Ser	Thr	Lys	Asp	Asn	Val	Val	Thr	Ile	Asp	Glu	Ile
	115					120						125			
Asn	Arg	Ala	Ile	Asn	Ser	Ala	Cys	Ala	Lys	Ala	Gly	Leu	Asp	Asn	Asp
	130				135						140				
Lys	His	Ile	Leu	His	Ala	Leu	Pro	Tyr	Arg	Phe	Thr	Leu	Asp	Lys	Gln
145				150					155					160	
Glu	Val	Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe
		165						170					175		
Ile	His	Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys
	180						185					190			
Ile	Met	Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser
	195					200						205			
Tyr	Ala	Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly
	210				215						220				
Val	Ala	Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr
225				230					235					240	
Ser	Gly	Asn	Ser	Ile	Arg	Tyr	Asn	Lys	Tyr	Leu	Pro	Val	Gly	Ser	His
		245						250					255		
His	Leu	Thr	Thr	Asp	Leu	Ser	His	Met	Leu	Asn	Thr	Pro	Phe	Pro	Tyr
		260					265						270		
Ala	Glu	Glu	Val	Lys	Ile	Lys	Tyr	Gly	Asp	Leu	Ser	Phe	Glu	Gly	Gly
	275					280						285			
Glu	Glu	Thr	Pro	Ser	Gln	Asn	Val	Gln	Ile	Pro	Thr	Thr	Gly	Ser	Asp
	290				295						300				
Gly	His	Glu	Ser	His	Ile	Val	Pro	Leu	Ser	Glu	Ile	Gln	Thr	Ile	Met
305				310					315					320	
Arg	Glu	Arg	Ala	Leu	Glu	Thr	Phe	Lys	Ile	Ile	His	Arg	Ser	Ile	Gln
		325						330					335		
Asp	Ser	Gly	Leu	Glu	Glu	His	Leu	Gly	Gly	Gly	Val	Val	Leu	Thr	Gly
		340					345						350		
Gly	Met	Ala	Leu	Met	Lys	Gly	Ile	Lys	Glu	Leu	Ala	Arg	Thr	His	Phe
	355					360						365			
Thr	Asn	Tyr	Pro	Val	Arg	Leu	Ala	Ala	Pro	Val	Glu	Lys	Tyr	Asn	Ile

370		375		380
Met Gly Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val				
385		390		400
Gly Leu Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp				
	405		410	415
Ser Lys Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr				
	420		425	430
Ala His Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu				
	435		440	445
Arg Asn Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala				
	450		455	460
Lys Asn Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe				
465		470		480
Phe Lys Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe				
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 <211> 1987
 <212> DNA
 <213> Helicobacter pylori

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 <222> (51)...(1934)

<400> 143
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 Met Ile
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 Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys
 5 10 15

ggc att gat ggc gca agc cct gaa gaa caa tta gaa aaa atc aag cat 152
 Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His
 20 25 30

tat tta gcg cat gaa att gaa gaa agg gag tta gaa ttc caa aaa atc 200
 Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln Lys Ile
 35 40 45 50

caa gcc cta ctc ttt aaa aaa ggg ctt tgt atc acc ccc tat aat gaa 248
 Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr Asn Glu
 55 60 65

ttg aat tta gag caa aaa gcg aag gct aaa acc tat ttt aaa gag cag 296
 Leu Asn Leu Glu Gln Lys Ala Lys Thr Tyr Phe Lys Glu Gln
 70 75 80

ctt tac gcg tta gtt ttg cct ttt aaa ttg gat tct tca cac act ttc 344
 Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His Thr Phe
 85 90 95

ccg cct tta gcg aat ttg act ttc gcg ctt ttt gcc cgc atc aaa gac	392
Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile Lys Asp	
100 105 110	
aaa gaa acc caa att atc tcc tat gcg ctc atc aaa ctc ccc tct ttt	440
Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro Ser Phe	
115 120 125 130	
atc ttc cgt ttt gta gag cta gaa aaa ggc ttg ttt gtg tta gct gaa	488
Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu Ala Glu	
135 140 145	
gaa atc gtg gaa gcg cat tta gaa gaa ttg ttt tta gag cat gag att	536
Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His Glu Ile	
150 155 160	
tta gat tgc atg gcg ttt agg gta act tgc gat gcg gat att gct atc	584
Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile Ala Ile	
165 170 175	
act gaa gat gaa gcg cat gat tat gca gat ttg atg agt aag agt ttg	632
Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys Ser Leu	
180 185 190	
agg aaa cgc aat caa ggc gaa atc gtg cgc ttg caa acc caa aaa ggg	680
Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln Lys Gly	
195 200 205 210	
agt caa gag ctt tta aaa acc ctc tta gcg tct tta agg agt ttt caa	728
Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser Phe Gln	
215 220 225	
acc cac tct tac aaa aag cac aaa ctc acc ggc atg cat atc tat aaa	776
Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile Tyr Lys	
230 235 240	
agc gcg atc atg ctc aat tta ggg gat ttg tgg gaa tta gtc aat cat	824
Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val Asn His	
245 250 255	
agc gat ttt aaa gcg ctc aaa tcg ccc aat ttc aca ccc aaa atc cac	872
Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys Ile His	
260 265 270	
cct cat ttc aat gaa aac gat ctt ttc aaa tct ata gaa aaa cag gat	920
Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp	
275 280 285 290	
ctg ttg ctg ttt cat cct tat gaa agt ttt gag cct gtg att gat tta	968
Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu	
295 300 305	
ata gag caa gcc gct agc gat cca gcc acc ctt tct atc aaa atg acg	1016
Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr	
310 315 320	

ctt tat cgt gtg ggc aag cat tcc ccc att gtc aaa gct ttg att gaa	1064
Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu	
325 330 335	
gcg gcg agc aag att caa gtg agc gtt tta gtg gaa tta aaa gcg cgc	1112
Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg	
340 345 350	
ttt gat gaa gag agc aat ctg cac tgg gca aaa gct tta gaa agg gcg	1160
Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala	
355 360 365 370	
ggc gcg tta gtc gtt tat ggc gtt ttc aaa ctc aaa gtg cat gct aaa	1208
Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys	
375 380 385	
atg cta ttg atc act aaa aaa aca gac aac caa tta cgc cat ttc acc	1256
Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr	
390 395 400	
cat tta agc acg ggc aat tac aac cct ttg agc gct aaa gtc tat acc	1304
His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val Tyr Thr	
405 410 415	
gat gtg agt ttt ttt agc gct aaa aat gaa atc gct aac gac att atc	1352
Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp Ile Ile	
420 425 430	
aag ctt ttc cat tcc ttg ctc act agc agc gcg act aat agc gca tta	1400
Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser Ala Leu	
435 440 445 450	
gaa acg ctt ttt atg gca ccc aaa caa atc aag cct aaa atc att gaa	1448
Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile Ile Glu	
455 460 465	
ctc att caa aat gaa atg aat cac caa caa gaa ggc tat atc att tta	1496
Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile Ile Leu	
470 475 480	
aaa gcc aac gcc cta gtg gat agc gaa atc att gaa tgg ctc tat caa	1544
Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu Tyr Gln	
485 490 495	
gcc tct caa aaa ggg gtt aaa att gat ctc att att aga ggg att tgc	1592
Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly Ile Cys	
500 505 510	
tgt tta aag ccc caa gtc aag ggc ttg agc gaa aat atc agg gtg tat	1640
Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg Val Tyr	
515 520 525 530	
tct atc gtg ggg aaa tat tta gaa cat gca cgc att tat tat ttt aaa	1688
Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr Phe Lys	

535	540	545	
cat gaa aat att tat ttt tct agc gcg gat tta atg ccc agg aat tta			1736
His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg Asn Leu			
550	555	560	
gaa agg cgc gtg gaa ttg ctc att cca gcc aca aac cca aag atc gct			1784
Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys Ile Ala			
565	570	575	
cat aaa ttg ttg cat att tta gaa atc caa ctc aaa gac acc tta aaa			1832
His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr Leu Lys			
580	585	590	
cgc tac gag tta aat tct aaa ggc cgt tac att aaa gtt tca aac cct			1880
Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser Asn Pro			
595	600	605	610
aac gat cct tta aat tgc cag gat tat ttt gaa aaa caa gcc ctt aaa			1928
Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala Leu Lys			
615	620	625	
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Thr Phe			
att			1987
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<211> 628			
<212> PRT			
<213> Helicobacter pylori			
<400> 144			
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Lys His Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln			
35 40 45			
Lys Ile Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr			
50 55 60			
Asn Glu Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys			
65 70 75 80			
Glu Gln Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His			
85 90 95			
Thr Phe Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile			
100 105 110			
Lys Asp Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro			
115 120 125			
Ser Phe Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu			
130 135 140			
Ala Glu Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His			
145 150 155 160			
Glu Ile Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile			

-181-

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Leu Lys Thr Phe
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Met Gly
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Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly
5 10 15

tgt gtg agc aat ttt aat gaa gac act tac acg cta gac tta gtt tta 152
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu
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gaa aaa aag atc caa gcc agc agg aaa ggt gaa atc acc caa gat aat 200
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn
35 40 45 50

gtg cct atc atc acg gct atc gct acg cat tta aac gat gtg gat agc 248
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser
55 60 65

ggc act tac tat gac cat gag tat ttt tta gtg gag att ttc acg caa 296
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln
70 75 80

aat aac gac tgg ata gat gat ggc tat att tct tat gaa ctt ttt ggc 344
Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly
85 90 95

aca aaa cct ata ggc tca gag cct tta tgg gtg cga gaa atc aca aaa 392
Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Lys
100 105 110

gat gaa ttt gat ggc att tta gaa acc acg aac agg tgg agc aga gct 440
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala
115 120 125 130

ttt ttg ctc gct ttt aac aaa ttg gat tat tta gcg gtt caa gaa gcc 488
Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala
135 140 145

aaa cta gag ctt gat gcc tat agt ttg ggc aag att gtt ttt aat ttc 536
 Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe
 150 155 160

gct tat caa gtc ccc cta cct caa ttt taatgcgctt agattacgcc 583
 Ala Tyr Gln Val Pro Leu Pro Gln Phe
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 Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln
 35 40 45
 Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val
 50 55 60
 Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe
 65 70 75 80
 Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu
 85 90 95
 Phe Gly Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile
 100 105 110
 Thr Lys Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser
 115 120 125
 Arg Ala Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln
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 Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe
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 Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe
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 cgagttttga gaattttaa tctatcaact ttatttatgg ggctaattggg agcggtaaga 180
 caaccacttc tagtttttta aaaaatctag ctgaaaatgg gattgaagac aagtttgcta 240

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 cgaacgagaa tttagaaaaa attgaaagca agaaagaatc aataaacaaa gagaatgaaa 420
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 aggattttgc tgataggtgt tgggaaaaac tttataagaa aaatgaagag gattttaaag 540
 aaacgctaga aggctttaag cgtaaagaga agtttaaaga aaaaatcctt aaggaatttg 600
 aaaacgataa atacaatcaa agcgaaatag taggggttaga aaaattaaag gaaaaaattg 660
 agattgtttt tgggtgaaaac caaacagaat tggcactatt ggaatgcaat ttaacagatt 720
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 ccattgcaga ttttaataaaa agattaagca atgaagattg ggtagctcaa ggtagagaat 840
 atataaaaga taatagtata tgccctttct gtcaaaaaga aaccattacc gaagaattta 900
 aaaaacaact agaattcttat tttgatacaa gttatcaaga atctattgaa acgatcaagg 960
 aaaag atg gaa gac tac gca agc aga acc gct gga gca ctg gag cga ctt 1010
 Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu
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gat aag att gtt gaa aca gaa cag aag aat caa caa act aaa ttg gac 1058
 Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp
 20 25 30

aca gaa aat ttg aaa ata att att gaa act ttg aga agt aaa atc aat 1106
 Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn
 35 40 45

ggg aat cag caa aag atg ctt gat aaa agt aaa gaa atg agc aga aat 1154
 Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn
 50 55 60

ttt aag ctt gat agc act aaa aac gag ata gac gca att aaa gat ttg 1202
 Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu
 65 70 75

att aaa aag gct aat gag caa ata gcc aat tat aat gag atg ata aag 1250
 Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys
 80 85 90 95

gat att gaa aaa cag aaa aag agt tgt aag gaa caa act tgg aaa ttt 1298
 Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe
 100 105 110

cta gtc aat gaa ttt aaa agt gat ata caa gaa tat aat aaa aag tat 1346
 Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr
 115 120 125

tgc ggt ttg gag aaa gga ata aac aat tta gag aaa gca att agt gaa 1394
 Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu
 130 135 140

aat caa gaa gag gta aag aaa tta gaa aat gaa att aag gaa tta gaa 1442
 Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu
 145 150 155

aaa act atg gta agc ata aag ccc att gtc aat gaa atc aat acg ctt 1490
 Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu
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tta aaa ggg tat gga ttc gcg aat ttt agt ttg gca tgc act gaa gat	1538
Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp	
180 185 190	
gaa aaa ttt tat cgt att caa aga gaa gat ggt caa tta gta gga gaa	1586
Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu	
195 200 205	
aca ctg agc gag ggt gaa gtt act ttc atc act ttc tta tat tat tat	1634
Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr	
210 215 220	
cat tta gca aaa ggc tct tta gaa gag aac gat ata tca aaa aat aag	1682
His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys	
225 230 235	
gtt tta gtg att gat gac ccc att tca agt ttg gat agc aat ata ttg	1730
Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu	
240 245 250 255	
ttt ata gtg agt gtt tta gtt aaa gat ctt atg aaa gaa gcc atg gaa	1778
Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu	
260 265 270	
gaa aaa aca aac atc aag caa gtt att ata cta acc cac aac aca tat	1826
Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr	
275 280 285	
ttt tac aag gaa att aca tta gaa tgt gat tta aaa cgc tat caa ggg	1874
Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly	
290 295 300	
aaa tat tct ttt tgg ata att aaa aag gat aat aat gtt tca aaa att	1922
Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile	
305 310 315	
aaa gat tat aaa gaa aat ccc att aaa aat tcc tat gaa ttg cta tgg	1970
Lys Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp	
320 325 330 335	
caa gaa gta aaa caa gca aaa gaa aat aat gct tct tgg gta tct tta	2018
Gln Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu	
340 345 350	
caa aat gtt atg cga aga att att gag tat tac ttt agg att tta ggc	2066
Gln Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly	
355 360 365	
ggt ttt aaa cat aat gat agc ttg agt gaa tgt ttt gaa aat att gaa	2114
Gly Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu	
370 375 380	
gaa aaa cga gtg tgt aat tct ttc att tca tgg ttt aat gat ggc tct	2162
Glu Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser	

385	390	395	
cat ggg att tca gat gat ttg ttt atg caa agt caa gat aca agt att	2210		
His Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile			
400 405 410 415			
gag aca tat tta aaa gtt ttt gaa aaa ata ttt aaa gaa acc ggt cat	2258		
Glu Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His			
420 425 430			
gaa gct cat tat aaa atg atg atg aga atg aag taattgaatt aaaaacaagg	2311		
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35 40 45			
Asn Gln Lys Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe			
50 55 60			
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile			
65 70 75 80			
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp			
85 90 95			
Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu			
100 105 110			
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys			
115 120 125			
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130 135 140			
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu Lys			
145 150 155 160			
Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu Leu			
165 170 175			
Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp Glu			
180 185 190			
Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu Thr			
195 200 205			
Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr His			
210 215 220			
Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys Val			
225 230 235 240			
Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu Phe			
245 250 255			
Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu Glu			

ggc ctt atc act tta agc tct caa acc gtc att gac gct tta ggc tat	296
Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr	
70 75 80	
ggc gtg agt aac act gtt ggc aac caa tta gag ggc att tct aat atc	344
Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile	
85 90 95	
ttg aat caa att ggc aaa aga aaa gac ttt tat tct agc cgt caa atc	392
Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile	
100 105 110	
tct agc att tcc caa caa atc ata ggg ctt aaa gga agc tct gat ccc	440
Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro	
115 120 125 130	
tta aaa gcc cat tct tca cag atc aca gcc aaa ctc ctt tcc aac acc	488
Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr	
135 140 145	
caa agc gcg ttt gat cag ggc atc gcg cta agc act aac atc att agc	536
Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser	
150 155 160	
tct atc aat agc cta aac cct agc aac aac acc caa gag gtt aaa aaa	584
Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys	
165 170 175	
cag ctc caa aac acc gcg caa tcc atg aca gaa ttg ttg caa caa att	632
Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile	
180 185 190	
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Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu	
195 200 205 210	
ctc tcc aat cta acc gat gcg gtg aat gcc tct agc aat aat acc gct	728
Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Ala	
215 220 225	
tat gtg agc gct ctt gtt aac gct tta aac act tta ggg gta ggg gtt	776
Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val	
230 235 240	
ttc ccc acc aca acc aca acg cat gtg gtg tta aac cca ccg gga caa	824
Phe Pro Thr Thr Thr Thr Thr His Val Val Leu Asn Pro Pro Gly Gln	
245 250 255	
gtc gta ttc tat cca acc aat tcc att tta ggc tct act tct tca aac	872
Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser Ser Asn	
260 265 270	
agc aat aac caa caa caa tac aac aac acc ctt tta atg aac acc tta	920
Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn Thr Leu	
275 280 285 290	

caa ggg aca tta agc gct aat act caa aat aac ccc aat ggt tgc gcc	968
Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly Cys Ala	
295 300 305	
aat caa gtc cag tgt ttg gag caa ttc atc caa aat tta gcc cct tta	1016
Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala Pro Leu	
310 315 320	
gcc gca acc ccc act tca aac aac cag gcc aac cag caa gtc caa gcc	1064
Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Gln Val Gln Ala	
325 330 335	
atc gct caa aag ctt caa agc gtt gct atc aac act tta gac aac aat	1112
Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp Asn Asn	
340 345 350	
gcg atc aac aac acc acc tat aat tta aac aat ttg cac aac gct ttg	1160
Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn Ala Leu	
355 360 365 370	
aat ttc caa gcc tat gaa agc acg ata gaa caa tac aat aac gct tta	1208
Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn Ala Leu	
375 380 385	
aaa caa att tct tgg atc agt ttt act gag cct aaa aac tta ctc aaa	1256
Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu Leu Lys	
390 395 400	
aac act tcc aat aac tac caa atc ggc acc gtt acc aac gct caa ggg	1304
Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala Gln Gly	
405 410 415	
caa aat atc agc gcc tat gat tgc atg act gct acc gga agc ctt tct	1352
Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser	
420 425 430	
agc aat gct tct agc ggg att tca tgc tca gcc aca agc tcc aca agt	1400
Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser	
435 440 445 450	
tcc aca aat agc ttt gac aat tct tta gtc gct acc tcc aaa gtc caa	1448
Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln	
455 460 465	
acc atc aac ggc aaa gag cag atc ggc gtg aat tct ttt aac ctt gtc	1496
Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val	
470 475 480	
tct caa gtg tgg agc gtt tat aat tct tta aaa act tca gaa gaa aat	1544
Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn	
485 490 495	
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gcc caa ttg caa aat Ala Gln Leu Gln Asn 535	att tta agc cct act Ile Leu Ser Pro Thr 540	agt ggg act acc act aat Ser Gly Thr Thr Thr Asn 545	1688
act caa gct aaa agc Thr Gln Ala Lys Ser 550	aac gct ccc aaa cta Asn Ala Pro Lys Leu 555	gcg atg gtg gtg gtg Ala Met Val Val Val 560	1736
aat aat gaa gaa gaa Asn Asn Glu Glu Glu 565	gct aaa acg gcc aat Ala Lys Thr Ala Asn 570	tta gcc caa agc agc ggg Leu Ala Gln Ser Ser Gly 575	1784
aca acc aca caa tct Thr Thr Thr Gln Ser 580	cct aac agc acg gtg Pro Asn Ser Thr Val 585	atg gga gct tta aac acc Met Gly Ala Leu Asn Thr 590	1832
gtg ttg caa aat gtc Val Leu Gln Asn Val 595	agc aat ttc caa caa Ser Asn Phe Gln Gln 600	agc att caa aac gct ttt Ser Ile Gln Asn Ala Phe 605	1880
caa aac caa gaa agt Gln Asn Gln Glu Ser 615	aat atc caa gct tgg Asn Ile Gln Ala Trp 620	gcg aat gcg att tat aac Ala Asn Ala Ile Tyr Asn 625	1928
act aat ggg agt cag Thr Asn Gly Ser Gln 630	tcg caa gag atg aca Ser Gln Glu Met Thr 635	cct aac aat aac caa gat Pro Asn Asn Asn Gln Asp 640	1976
tta cgc atc caa ttg Leu Arg Ile Gln Leu 645	agg gcg aat ttt tac Arg Ala Asn Phe Tyr 650	cag ctc atc aat acc att Gln Leu Ile Asn Thr Ile 655	2024
aac cag caa gtg cct Asn Gln Gln Val Pro 660	aca gac atg aat gct Thr Asp Met Asn Ala 665	tta att aat caa agc caa Leu Ile Asn Gln Ser Gln 670	2072
caa acc caa caa aca Gln Thr Gln Gln Thr 675	agc gga tca gca agc Ser Gly Ser Ala Ser 680	aat aat aac gca tgc gcg Asn Asn Asn Ala Cys Ala 685	2120
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gat tct aag gct tat Asp Ser Lys Ala Tyr 710	tac agc ggg ttg caa Tyr Ser Gly Leu Gln 715	agc gct tta ggg tat caa Ser Ala Leu Gly Tyr Gln 720	2216
acg caa gcg aca act acg caa agc ggg agc aat ggt ggg aac agc atc acc			2264

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tac	aat	gtc	caa	caa	atc	acg	ctc	act	agt	aat	ggt	ttg	ctc	aac	caa	2312	
Tyr	Asn	Val	Gln	Gln	Ile	Thr	Leu	Thr	Ser	Asn	Gly	Leu	Leu	Asn	Gln		
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atc	atc	aca	aat	ctt	aag	agc	gtt	aat	gga	ggc	aat	ggc	gcg	agt	ggt	2360	
Ile	Ile	Thr	Asn	Leu	Lys	Ser	Val	Asn	Gly	Gly	Asn	Gly	Ala	Ser	Gly		
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Thr	Gly	Ser	Gly	Asn	Gly	Thr	Ser	Gln	Ile	Asn	Thr	Ala	Tyr	Gln	Met		
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ctc	aca	gac	gcc	agc	gat	ggg	aaa	tta	ggg	act	tat	agt	agt	agt	agt	2456	
Leu	Thr	Asp	Ala	Ser	Asp	Gly	Lys	Leu	Gly	Thr	Tyr	Ser	Ser	Ser	Ser		
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Lys	Thr	Ser	Gly	Asn	Asn	Cys	Tyr	Glu	Pro	Asn	Lys	Gln	Gln	Asn	Ala		
	820					825					830						
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Thr	Thr	Ala	Thr	Ala	Thr	Thr	Asp	Ser	Asn	Leu	Gln	Lys	Val	Tyr	Asn		
	835				840					845					850		
gac	gcc	caa	aaa	ata	gcc	aac	att	atc	gcc	agc	tct	ggg	aac	aat	aaa	2648	
Asp	Ala	Gln	Lys	Ile	Ala	Asn	Ile	Ile	Ala	Ser	Ser	Gly	Asn	Asn	Lys		
				855					860					865			
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Gly	Val	Glu	Asn	Gly	Leu	Lys	Gln	Phe	Phe	Glu	Ala	Leu	Lys	Asn	Asn		
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agc	agc	agt	ctc	agt	aat	tta	tgt	ggt	aat	ggt	agt	agc	ggt	agt	agt	2744	
Ser	Ser	Ser	Leu	Ser	Asn	Leu	Cys	Gly	Asn	Gly	Ser	Ser	Gly	Ser	Ser		
		885				890						895					
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Gly	Thr	Thr	Cys	Ser	Gly	Trp	Leu	Ile	Asn	Leu	Leu	Gly	Ala	Ile	Pro		
	900					905					910						
acc	aat	gga	gtg	agc	gat	acg	aat	aat	tta	att	aat	ctg	ctc	act	gaa	2840	
Thr	Asn	Gly	Val	Ser	Asp	Thr	Asn	Asn	Leu	Ile	Asn	Leu	Leu	Thr	Glu		
	915				920					925					930		
ttc	att	aaa	acc	gcc	ggg	ttt	atc	caa	aat	aat	gat	agt	agt	gta	tct	2888	
Phe	Ile	Lys	Thr	Ala	Gly	Phe	Ile	Gln	Asn	Asn	Asp	Ser	Ser	Val	Ser		
				935					940					945			

act agt ctt aca agc gct ttt caa gcc att acg agc gct att tct caa	2936
Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln	
950 955 960	
ggg ttt caa gcc tta caa aac gat att agc cct aat gcg att tta acc	2984
Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr	
965 970 975	
ttg ctc caa gag att act tct aac acc acc acc att cag tca ttc tcg	3032
Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser	
980 985 990	
caa acc tta cgg cag ctt tta ggg gat aaa aca ttc ttt atg gcg caa	3080
Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr Phe Phe Met Ala Gln	
995 1000 1005 1010	
caa aag ctc att gat gcg atg att aac gcc aga aat cag gtt caa aac	3128
Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg Asn Gln Val Gln Asn	
1015 1020 1025	
gcg caa aat caa gcc aat aac tac ggc tct caa ccc gtt tta agc cag	3176
Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln Pro Val Leu Ser Gln	
1030 1035 1040	
tat gcg gcc gct aaa agc acc caa cat ggc atg agc aat ggt tta ggg	3224
Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly Leu Gly	
1045 1050 1055	
gtt ggt ttg ggc tat aaa tac ttc ttt ggt aaa gcg aga aaa tta ggc	3272
Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys Leu Gly	
1060 1065 1070	
ctt agg cat tat ttt ttc ttt gat tac ggc ttt agt gaa ata ggc cta	3320
Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile Gly Leu	
1075 1080 1085 1090	
gcc aat caa agc gtg aaa gcg aat atc ttt gct tat ggg gta ggc acg	3368
Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val Gly Thr	
1095 1100 1105	
gat ttt tta tgg aac tta ttc agg agg act tac aac act aaa gcg ttg	3416
Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys Ala Leu	
1110 1115 1120	
aat ttt ggg cta ttt gct ggg gtc caa ctg ggc ggc gca acc tgg ctt	3464
Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr Trp Leu	
1125 1130 1135	
agc tcc tta agg caa caa atc att gac aac tgg ggg agt gct aat gac	3512
Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala Asn Asp	
1140 1145 1150	
atc cat tca acg aat ttt caa gtg gcg ctg aat ttt ggg gtg cgc acc	3560
Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val Arg Thr	
1155 1160 1165 1170	

aac ttc gcg gag ttt aag cgt ttt gct aag aaa ttc cac aat caa ggg 3608
 Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn Gln Gly
 1175 1180 1185

gtc atc agc caa aag agc gtg gaa ttt ggg atc aaa gtg cct ctc atc 3656
 Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro Leu Ile
 1190 1195 1200

aat caa gcg tat ttg aat agc gct gga gct gat gtg agt tac agg agg 3704
 Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr Arg Arg
 1205 1210 1215

ctt tat act ttt tat atc aat tac atc atg ggg ttt taaaaaagg 3750
 Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
 1220 1225 1230

tgtgtcatgg aaatcttaca attcatcggc tatgggaata tgg 3793

<210> 150

<211> 1230

<212> PRT

<213> Helicobacter pylori

<400> 150

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 1 5 10 15
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 20 25 30
 Gly Gly Thr Gln Gln Phe Ile Asn Lys Gln Leu Leu Glu Asn Gln
 35 40 45
 Asn Ile Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro
 50 55 60
 Thr Thr Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu
 65 70 75 80
 Gly Tyr Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser
 85 90 95
 Asn Ile Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg
 100 105 110
 Gln Ile Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser
 115 120 125
 Asp Pro Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser
 130 135 140
 Asn Thr Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile
 145 150 155 160
 Ile Ser Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val
 165 170 175
 Lys Lys Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln
 180 185 190
 Gln Ile Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln
 195 200 205
 Ser Leu Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn
 210 215 220
 Thr Ala Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val
 225 230 235 240

Gly	Val	Phe	Pro	Thr	Thr	Thr	Thr	Thr	His	Val	Val	Leu	Asn	Pro	Pro	
				245					250					255		
Gly	Gln	Val	Val	Phe	Tyr	Pro	Thr	Asn	Ser	Ile	Leu	Gly	Ser	Thr	Ser	
			260					265					270			
Ser	Asn	Ser	Asn	Asn	Gln	Gln	Gln	Tyr	Asn	Asn	Thr	Leu	Leu	Met	Asn	
		275					280					285				
Thr	Leu	Gln	Gly	Thr	Leu	Ser	Ala	Asn	Thr	Gln	Asn	Asn	Pro	Asn	Gly	
	290					295					300					
Cys	Ala	Asn	Gln	Val	Gln	Cys	Leu	Glu	Gln	Phe	Ile	Gln	Asn	Leu	Ala	
305					310					315					320	
Pro	Leu	Ala	Ala	Thr	Pro	Thr	Ser	Asn	Asn	Gln	Ala	Asn	Gln	Gln	Val	
			325						330					335		
Gln	Ala	Ile	Ala	Gln	Lys	Leu	Gln	Ser	Val	Ala	Ile	Asn	Thr	Leu	Asp	
		340					345						350			
Asn	Asn	Ala	Ile	Asn	Asn	Thr	Thr	Tyr	Asn	Leu	Asn	Asn	Leu	His	Asn	
		355				360						365				
Ala	Leu	Asn	Phe	Gln	Ala	Tyr	Glu	Ser	Thr	Ile	Glu	Gln	Tyr	Asn	Asn	
	370					375				380						
Ala	Leu	Lys	Gln	Ile	Ser	Trp	Ile	Ser	Phe	Thr	Glu	Pro	Lys	Asn	Leu	
385					390				395						400	
Leu	Lys	Asn	Thr	Ser	Asn	Asn	Tyr	Gln	Ile	Gly	Thr	Val	Thr	Asn	Ala	
			405					410						415		
Gln	Gly	Gln	Asn	Ile	Ser	Ala	Tyr	Asp	Cys	Met	Thr	Ala	Thr	Gly	Ser	
		420					425						430			
Leu	Ser	Ser	Asn	Ala	Ser	Ser	Gly	Ile	Ser	Cys	Ser	Ala	Thr	Ser	Ser	
	435					440						445				
Thr	Ser	Ser	Thr	Asn	Ser	Phe	Asp	Asn	Ser	Leu	Val	Ala	Thr	Ser	Lys	
	450				455					460						
Val	Gln	Thr	Ile	Asn	Gly	Lys	Glu	Gln	Ile	Gly	Val	Asn	Ser	Phe	Asn	
465				470					475						480	
Leu	Val	Ser	Gln	Val	Trp	Ser	Val	Tyr	Asn	Ser	Leu	Lys	Thr	Ser	Glu	
			485					490						495		
Glu	Asn	Leu	Gln	Lys	Asn	Ala	Asn	Ile	Leu	Cys	Ala	Asn	Gly	Thr	Gln	
		500					505						510			
Ser	Gly	Thr	Ser	Ser	Cys	Asn	Ser	Ser	Ser	Gly	Gly	Leu	Ser	Ile	Ser	
	515					520						525				
Gly	Asn	Ala	Gln	Leu	Gln	Asn	Ile	Leu	Ser	Pro	Thr	Ser	Gly	Thr	Thr	
	530				535					540						
Thr	Asn	Thr	Gln	Ala	Lys	Ser	Asn	Ala	Pro	Lys	Leu	Lys	Ala	Met	Val	
545				550					555						560	
Val	Val	Asn	Asn	Glu	Glu	Glu	Ala	Lys	Thr	Ala	Asn	Leu	Ala	Gln	Ser	
			565				570							575		
Ser	Gly	Thr	Thr	Thr	Gln	Ser	Pro	Asn	Ser	Thr	Val	Met	Gly	Ala	Leu	
		580				585						590				
Asn	Thr	Val	Leu	Gln	Asn	Val	Ser	Asn	Phe	Gln	Gln	Ser	Ile	Gln	Asn	
	595					600						605				
Ala	Phe	Gln	Asn	Gln	Glu	Ser	Asn	Ile	Gln	Ala	Trp	Ala	Asn	Ala	Ile	
	610				615					620						
Tyr	Asn	Thr	Asn	Gly	Ser	Gln	Ser	Gln	Glu	Met	Thr	Pro	Asn	Asn	Asn	
625				630					635						640	
Gln	Asp	Leu	Arg	Ile	Gln	Leu	Arg	Ala	Asn	Phe	Tyr	Gln	Leu	Ile	Asn	
			645				650							655		
Thr	Ile	Asn	Gln	Gln	Val	Pro	Thr	Asp	Met	Asn	Ala	Leu	Ile	Asn	Gln	
		660					665					670				
Ser	Gln	Gln	Thr	Gln	Gln	Thr	Ser	Gly	Ser	Ala	Ser	Asn	Asn	Asn	Ala	

Ala Leu Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr
1125 1130 1135
Trp Leu Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala
1140 1145 1150
Asn Asp Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val
1155 1160 1165
Arg Thr Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn
1170 1175 1180
Gln Gly Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro
1185 1190 1195 1200
Leu Ile Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr
1205 1210 1215
Arg Arg Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
1220 1225 1230

<210> 151
<211> 1259
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (48)...(1226)

<400> 151
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Met Asn Lys
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aaa gcg tat ttt ggg gag ttt gga ggg agt ttt gtt tcg gag ttg tta 104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
5 10 15
gtg cct gca tta aga gaa tta gaa cag gcg ttt gat gcg tgt ttg aaa 152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
20 25 30 35
gat gaa aaa ttc caa aaa gaa tat ttt cgt ctt tta aag gat ttt gtg 200
Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val
40 45 50
ggc cgt cct agc cct tta acc ttg tgt caa aat atc gtt tct aac cct 248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro
55 60 65
aaa gtc aag ctt tat tta aaa cga gag gat tta atc cat ggc ggg geg 296
Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala
70 75 80
cat aag act aat caa gcc tta ggg caa gcc ctt tta gcg aaa aaa atg 344
His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met
85 90 95
ggt aaa aca agg atc atc gct gaa aca ggc gcc ggt cag cat ggc gtg 392

Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Val	
100					105					110					115	
gcg	acg	gct	atc	gct	tgc	gca	tta	ttg	aac	tta	aaa	tgc	gtg	gtt	ttt	440
Ala	Thr	Ala	Ile	Ala	Cys	Ala	Leu	Leu	Asn	Leu	Lys	Cys	Val	Val	Phe	
				120					125					130		
atg	gga	tct	aaa	gac	atc	aag	cgc	cag	gaa	atg	aat	gtt	ttt	aga	atg	488
Met	Gly	Ser	Lys	Asp	Ile	Lys	Arg	Gln	Glu	Met	Asn	Val	Phe	Arg	Met	
			135					140					145			
cac	tta	tta	ggc	gct	gaa	gtg	aga	gag	gtt	aat	tca	ggg	agc	gcg	acg	536
His	Leu	Leu	Gly	Ala	Glu	Val	Arg	Glu	Val	Asn	Ser	Gly	Ser	Ala	Thr	
			150					155				160				
ctt	aaa	gac	gct	gtg	aat	gaa	gcc	tta	aga	gat	tgg	gcg	agc	agt	tac	584
Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Ala	Ser	Ser	Tyr	
	165					170					175					
aag	gac	acg	cat	tat	ttg	cta	ggc	aca	gcc	gcc	ggg	cca	cac	cct	tac	632
Lys	Asp	Thr	His	Tyr	Leu	Leu	Gly	Thr	Ala	Ala	Gly	Pro	His	Pro	Tyr	
180					185					190					195	
ccc	aca	atg	gtt	aaa	acc	ttt	caa	aaa	atg	ata	ggc	gat	gag	gtt	aaa	680
Pro	Thr	Met	Val	Lys	Thr	Phe	Gln	Lys	Met	Ile	Gly	Asp	Glu	Val	Lys	
				200					205					210		
agc	cag	att	tta	gaa	aaa	gaa	aac	cgc	ttg	cct	gat	tat	gtg	atc	gca	728
Ser	Gln	Ile	Leu	Glu	Lys	Glu	Asn	Arg	Leu	Pro	Asp	Tyr	Val	Ile	Ala	
			215					220					225			
tgc	gtt	gga	ggg	ggg	tct	aac	gct	ata	ggg	ata	ttc	agc	gca	ttt	tta	776
Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Ile	Phe	Ser	Ala	Phe	Leu	
		230					235					240				
aac	gac	aaa	gaa	gtt	aaa	ctc	ata	ggc	gta	gag	ccg	gcg	ggg	tta	ggg	824
Asn	Asp	Lys	Glu	Val	Lys	Leu	Ile	Gly	Val	Glu	Pro	Ala	Gly	Leu	Gly	
	245					250					255					
cta	gaa	acc	aat	aag	cat	ggg	gcg	act	ttg	aat	aag	ggg	cgt	gtg	ggg	872
Leu	Glu	Thr	Asn	Lys	His	Gly	Ala	Thr	Leu	Asn	Lys	Gly	Arg	Val	Gly	
260					265				270					275		
att	ttg	cat	ggg	aat	aaa	acc	tat	ctt	tta	caa	gat	gat	gaa	ggc	cag	920
Ile	Leu	His	Gly	Asn	Lys	Thr	Tyr	Leu	Leu	Gln	Asp	Asp	Glu	Gly	Gln	
				280					285					290		
att	gca	gaa	agc	cat	agc	att	agc	gcc	ggg	ctt	gat	tat	cca	gga	gtg	968
Ile	Ala	Glu	Ser	His	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	Val	
			295					300					305			
ggg	cca	gaa	cac	agc	tat	tta	aaa	gaa	agt	ggg	cgt	gcg	gtt	tat	gaa	1016
Gly	Pro	Glu	His	Ser	Tyr	Leu	Lys	Glu	Ser	Gly	Arg	Ala	Val	Tyr	Glu	
		310					315					320				

agc gca agc gat gct gaa gcg cta gaa gcc ttc aag ttg ttg tgc caa 1064
 Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln
 325 330 335

aaa gaa ggc att atc cca gcg cta gaa agc tca cac gcc tta gcg tat 1112
 Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr
 340 345 350 355

gcc tta aag ctc gct caa aaa tgc gaa gaa gaa agc atc atc gta gtg 1160
 Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val
 360 365 370

aat tta agc ggc aga ggg gat aag gat tta agc acc gtt tat aac gct 1208
 Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala
 375 380 385

tta aaa gga ggt tta aaa tgaggatatca aaacatgttt gaaaccttaa 1256
 Leu Lys Gly Gly Leu Lys
 390

aaa 1259

<210> 152
 <211> 393
 <212> PRT
 <213> Helicobacter pylori

<400> 152
 Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser
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 Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala
 20 25 30
 Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys
 35 40 45
 Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val
 50 55 60
 Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His
 65 70 75 80
 Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala
 85 90 95
 Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln
 100 105 110
 His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys
 115 120 125
 Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val
 130 135 140
 Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly
 145 150 155 160
 Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala
 165 170 175
 Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro
 180 185 190
 His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp
 195 200 205
 Glu Val Lys Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr

210		215		220
Val Ile Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser				
225		230		235
Ala Phe Leu Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala				
	245		250	255
Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly				
	260		265	270
Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp				
	275		280	285
Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr				
	290		295	300
Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala				
305		310		315
Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu				
	325		330	335
Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala				
	340		345	350
Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile				
	355		360	365
Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val				
	370		375	380
Tyr Asn Ala Leu Lys Gly Gly Leu Lys				
385		390		

<210> 153
 <211> 601
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (197)...(547)

<221> misc_feature
 <222> 159
 <223> n = A,T,C or G

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 gtgggggtgat cccccctatt ttgcgttcag ctttgctcgt gttcccttct acgattttgc 120
 agcaagccac aagcaacaaa accttgcaag cggttgcgna ttttttaagc ccgcaaggta 180
 tgcgtataat attttg atg ttc ttg ctc atc atc ttt ttt gct tac ttt tat 232
 Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr
 1 5 10

 tct tct att gtg ttc aat tct aag gat att gcg gat aat ttg agg cgt 280
 Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg
 15 20 25

 aat ggc ggg tat att cca ggg ctt agg cct gga gag ggg act tca tcg 328
 Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser
 30 35 40

 ttt tta aat tct gta gcg agt aag ctc act ttg tgg ggt tca ttg tat 376

Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr
45 50 55 60
tta gcg ctc att tct acc gtg cct tgg att ttg gtt aag gct atg ggc 424
Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly
65 70 75
gtg cct ttt tac ttt gga ggc aca gcg gtg ctg att gtg gtt caa gtc 472
Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val
80 85 90
gct att gac acc atg aaa aag att gaa gcg caa att tat atg agc aag 520
Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys
95 100 105
tat aaa act tta agc gcg gta ggc ttt taatggcaat ctctattaaa 567
Tyr Lys Thr Leu Ser Ala Val Gly Phe
110 115
agcccaaaag aaatcaaagc tctaagaaaa gccg 601
<210> 154
<211> 117
<212> PRT
<213> Helicobacter pylori
<400> 154
Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr Ser Ser Ile Val
1 5 10 15
Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg Asn Gly Gly Tyr
20 25 30
Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser Phe Leu Asn Ser
35 40 45
Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr Leu Ala Leu Ile
50 55 60
Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly Val Pro Phe Tyr
65 70 75 80
Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val Ala Ile Asp Thr
85 90 95
Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys Tyr Lys Thr Leu
100 105 110
Ser Ala Val Gly Phe
115
<210> 155
<211> 725
<212> DNA
<213> Helicobacter pylori
<220>
<221> CDS
<222> (64)...(675)
<400> 155

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tca atg act cta ggc att gat gaa gcg ggt agg ggg tgt ttg gcc ggt	108
Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly	
1 5 10 15	
tcg ctt ttt gtg gct ggg gtg gcg tgt aat gaa aaa aca gcc tta gaa	156
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu	
20 25 30	
ttt cta aaa atg ggt tta aaa gac agc aag aag ctc agc cta aaa aag	204
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys	
35 40 45	
cgc ttt ttc tta gaa tat aag atc aaa acg cat ggt gag gtg ggg ttt	252
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe	
50 55 60	
ttc gtg gtt aaa aaa agc gca aat gaa att gat agc ttg ggc tta ggg	300
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly	
65 70 75	
gcg tgt ttg aaa ctc gct gtg caa gaa att tta gaa aat ggt tgc tct	348
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser	
80 85 90 95	
tta gtt gat gaa ata aaa ata gac ggc aac acg gcg ttt ggc ttg aac	396
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn	
100 105 110	
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Lys Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile	
115 120 125	
gct caa atc gct atg gcg tct gtt ttg gcg aaa gct ttt aag gac aga	492
Ala Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg	
130 135 140	
gaa atg cta gag ttg cac gct ttg ttt aag gaa tac ggc tgg gat aag	540
Glu Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys	
145 150 155	
aat tgc ggg tat ggg act aaa caa cat ata gaa gcg atc att aag cta	588
Asn Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu	
160 165 170 175	
ggg gct acg cct ttt cat cgg cat agc ttc acg ctt aaa aac cgc atc	636
Gly Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile	
180 185 190	
tta aat ccc aaa ctc tta gag gtg gaa caa cgc ctt att taaaagggcg	685
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 35 40 45
 Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe Phe
 50 55 60
 Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly Ala
 65 70 75 80
 Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser Leu
 85 90 95
 Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn Lys
 100 105 110
 Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile Ala
 115 120 125
 Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg Glu
 130 135 140
 Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys Asn
 145 150 155 160
 Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu Gly
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 Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp Gln
 5 10 15
 gag caa caa gcg ttt aaa cgc atg caa gct agg aaa gac aac cat ggg 156
 Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His Gly
 20 25 30

gat ttc act ttg cat gac ggg ccg cct tat gcg aac ggg cat ttg cat	204
Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu His	
35 40 45	
ttg ggg cat gcc tta aat aaa att tta aaa gac att gtc gtt aaa aga	252
Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys Arg	
50 55 60 65	
gaa tat ttt aag ggg aag aaa atc tat tac acg ccc ggt tgg gat tgc	300
Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp Cys	
70 75 80	
cat ggt ttg ccc att gag cag caa att tta gag cga tta gaa aaa gaa	348
His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys Glu	
85 90 95	
aaa aca agc cta gaa aac ccc acg ctg ttt aga gaa aag tgc cga gat	396
Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg Asp	
100 105 110	
cat gcg aag aaa ttt tta gaa atc caa aag aat gaa ttt ttg caa ttg	444
His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln Leu	
115 120 125	
ggt gtt ttg ggg gat ttt gaa gat cct tat aaa acc atg gat ttt aaa	492
Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe Lys	
130 135 140 145	
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Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys Gly	
150 155 160	
ctt ttg aaa gag cgc cac aag cct att tat tgg agt tat gca tgc gag	588
Leu Leu Lys Glu Arg His Lys Pro Ile Tyr Trp Ser Tyr Ala Cys Glu	
165 170 175	
agc gct tta gcg gaa gct gaa gtg gaa tac aaa atg aaa aaa tcg ccc	636
Ser Ala Leu Ala Glu Ala Glu Val Glu Tyr Lys Met Lys Lys Ser Pro	
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tcc att ttc gtg gcg ttt ggt ttg aaa aag gag agt tta gaa aaa tta	684
Ser Ile Phe Val Ala Phe Gly Leu Lys Lys Glu Ser Leu Glu Lys Leu	
195 200 205	
aaa gtc aaa aaa gcg agc ttg gtg att tgg acg acc acg cct tgg act	732
Lys Val Lys Lys Ala Ser Leu Val Ile Trp Thr Thr Thr Pro Trp Thr	
210 215 220 225	
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Leu Tyr Ala Asn Val Ala Ile Ala Leu Lys Lys Asp Ala Val Tyr Ala	
230 235 240	
ctc acc caa aaa ggc tat tta gtc gct aaa gcc ttg cat gaa aaa tta	828
Leu Thr Gln Lys Gly Tyr Leu Val Ala Lys Ala Leu His Glu Lys Leu	

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gcc gct tta ggg gtg gtg gat aat gag atc aca cat gaa ttc aat tcc			876
Ala Ala Leu Gly Val Val Asp Asn Glu Ile Thr His Glu Phe Asn Ser			
260	265	270	
aat gat tta gaa tat tta gtg gct aca aac ccg ctc aat caa agg gat			924
Asn Asp Leu Glu Tyr Leu Val Ala Thr Asn Pro Leu Asn Gln Arg Asp			
275	280	285	
tcg ctg gtg gct tta gga gag cat gtc ggt tta gaa gat ggc aca gga			972
Ser Leu Val Ala Leu Gly Glu His Val Gly Leu Glu Asp Gly Thr Gly			
290	295	300	305
gcc gtg cat acc gca cct ggg cat ggt gaa gag gac tat tat tta ggc			1020
Ala Val His Thr Ala Pro Gly His Gly Glu Glu Asp Tyr Tyr Leu Gly			
310	315	320	
tta aga tat aat tta gaa gtg tta atg tct gta gat gag aaa ggt tgc			1068
Leu Arg Tyr Asn Leu Glu Val Leu Met Ser Val Asp Glu Lys Gly Cys			
325	330	335	
tat gat gag ggc att atc cat aac caa cta tta gat gaa agc tat ctg			1116
Tyr Asp Glu Gly Ile Ile His Asn Gln Leu Leu Asp Glu Ser Tyr Leu			
340	345	350	
ggc gag cat gtt ttt aag gct caa aaa cgc att ata gag caa ttg ggc			1164
Gly Glu His Val Phe Lys Ala Gln Lys Arg Ile Ile Glu Gln Leu Gly			
355	360	365	
gat tct tta ttg cta gag caa gag att gag cat tct tat ccg cat tgc			1212
Asp Ser Leu Leu Leu Glu Gln Glu Ile Glu His Ser Tyr Pro His Cys			
370	375	380	385
tgg agg acg cac aag cct gtg att tac aga gcg act acg caa tgg ttt			1260
Trp Arg Thr His Lys Pro Val Ile Tyr Arg Ala Thr Thr Gln Trp Phe			
390	395	400	
att tta atg gat gag cct ttt atc caa aat gat ggc tct caa aaa acc			1308
Ile Leu Met Asp Glu Pro Phe Ile Gln Asn Asp Gly Ser Gln Lys Thr			
405	410	415	
tta aga gaa gtg gct tta gat gcg att gaa aag gtg gaa ttt gtg cca			1356
Leu Arg Glu Val Ala Leu Asp Ala Ile Glu Lys Val Glu Phe Val Pro			
420	425	430	
agc agc ggg aaa aac cgc cta aaa acc atg ata gaa aac cgc cct gat			1404
Ser Ser Gly Lys Asn Arg Leu Lys Thr Met Ile Glu Asn Arg Pro Asp			
435	440	445	
tgg tgc ttg agc cgg caa aga aaa tgg ggc gtg cca ctg gcc ttt ttc			1452
Trp Cys Leu Ser Arg Gln Arg Lys Trp Gly Val Pro Leu Ala Phe Phe			
450	455	460	465
ata gac aaa cgc acg aat aag cct tgt ttt gaa agc gaa gtt tta gag			1500

Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	Glu		
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cat	gtg	gcc	aat	ctt	ttt	gag	aaa	aaa	ggc	tgt	gat	gtg	tgg	tgg	gag	1548	
His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	Glu		
			485					490					495				
tat	agc	gtg	aaa	gat	tta	ttg	ccc	cct	agc	tat	caa	gag	gac	gcc	aag	1596	
Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	Lys		
		500					505					510					
cat	tat	gag	aaa	atc	atg	cac	att	tta	gac	gtg	tgg	ttt	gat	agt	ggc	1644	
His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	Gly		
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Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly	Gln		
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agc	cct	agc	gat	gtg	atc	tta	gaa	ggg	agc	gat	cag	cat	agg	ggg	tgg	1740	
Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	Trp		
				550					555					560			
ttt	caa	agc	tcg	ctt	cta	atc	ggc	tgt	gtt	tta	aac	aac	caa	gcc	cct	1788	
Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	Pro		
			565					570					575				
ttt	aaa	aag	gtc	att	acg	cat	ggc	ttt	atc	gta	gat	gaa	aag	ggc	gaa	1836	
Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	Glu		
		580					585					590					
aaa	atg	agt	aaa	tct	aag	ggc	aat	gtg	gtg	tct	ttg	gac	aag	ctg	ctc	1884	
Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	Leu		
	595					600					605						
aaa	acg	cat	ggg	agc	gat	gtg	gtg	cgt	ttg	tgg	gta	gcg	ttt	aat	gac	1932	
Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn	Asp		
610					615					620					625		
tat	caa	aac	gat	ttg	aga	gtc	tct	caa	acc	ttt	ttc	act	caa	aca	gaa	1980	
Tyr	Gln	Asn	Asp	Leu	Arg	Val	Ser	Gln	Thr	Phe	Phe	Thr	Gln	Thr	Glu		
				630					635					640			
caa	cat	tat	aaa	aaa	ttc	cgc	aac	acc	ctg	aaa	ttc	tta	ctc	gct	aat	2028	
Gln	His	Tyr	Lys	Lys	Phe	Arg	Asn	Thr	Leu	Lys	Phe	Leu	Leu	Ala	Asn		
			645					650					655				
ttt	agc	gat	atg	gat	ctc	aag	aat	tta	gaa	cgc	ccc	cat	aac	ttc	agc	2076	
Phe	Ser	Asp	Met	Asp	Leu	Lys	Asn	Leu	Glu	Arg	Pro	His	Asn	Phe	Ser		
		660					665					670					
cct	tta	gat	cat	ttt	atg	tta	gag	act	tta	gaa	acc	ata	agc	gct	gga	2124	
Pro	Leu	Asp	His	Phe	Met	Leu	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Ala	Gly		
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gtc aat agc gcg ttt gaa gag cat gat ttt gtg aaa ggc ttg aat att	2172
Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn Ile	
690 695 700 705	
tta atg gcg ttt gtt acc aat gaa ttg agc ggg att tat tta gac gct	2220
Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp Ala	
710 715 720	
tgc aag gat agc ttg tat tgc gat agc aaa aac aat gaa aaa cgc caa	2268
Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg Gln	
725 730 735	
gcc att caa atg gtt tta ctc gct aca gct agt aag ttg tgc tac ttt	2316
Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr Phe	
740 745 750	
tta gcc ccg att tta acg cac acg att gaa gaa gtt tta gag cat agc	2364
Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His Ser	
755 760 765	
caa gcg ctt cgc att ttt tta caa gcc aaa gat gtg ttt gat tta aaa	2412
Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu Lys	
770 775 780 785	
gac att agc gtt tca gaa aaa ctc cac ctc aaa gag ttt aaa aaa cca	2460
Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys Pro	
790 795 800	
gaa aat ttt gaa gcc gtt tta gcc ttg cgt tct gcc ttt aat gaa gag	2508
Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu Glu	
805 810 815	
tta gac cga ttg aaa aaa gaa ggc gtc att aaa aat tgc tta gag tgc	2556
Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu Cys	
820 825 830	
gct att gaa gta aaa gaa aaa gcg ttg gat gaa aat tta gta gaa gag	2604
Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu Glu	
835 840 845	
ttg ctg atg gta agc ttt gtg ggg att gca aaa gaa aaa ttg agt gaa	2652
Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser Glu	
850 855 860 865	
acg cca gca ttc acg ctc ttt aaa gcc ccc ttt tat aaa tgc ccc agg	2700
Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro Arg	
870 875 880	
tgt tgg cgt ttt aaa agc gag cta gaa aac acc cct tgc aag cgt tgc	2748
Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg Cys	
885 890 895	
gaa cag gtt tta aaa gag cga tgataaaagg atagggcttt tgaaaacttt	2799
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2821

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<211> 904

<212> PRT

<213> Helicobacter pylori

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Gly	Asp	Phe	Thr	Leu	His	Asp	Gly	Pro	Pro	Tyr	Ala	Asn	Gly	His	Leu
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Cys	His	Gly	Leu	Pro	Ile	Glu	Gln	Gln	Ile	Leu	Glu	Arg	Leu	Glu	Lys
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	130					135					140				
Lys	Phe	Glu	Ala	Ser	Ile	Tyr	Arg	Ala	Leu	Val	Glu	Val	Ala	Lys	Lys
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Gly	Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys
			165					170						175	
Glu	Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser
			180					185					190		
Pro	Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys
		195					200					205			
Leu	Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp
	210					215					220				
Thr	Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr
225					230					235					240
Ala	Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys
			245						250					255	
Leu	Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn
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	275						280					285			
Asp	Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr
	290					295					300				
Gly	Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu
305					310					315					320
Gly	Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly
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Cys	Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr
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		355					360						365		

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	370						375				380					
Cys	Trp	Arg	Thr	His	Lys	Pro	Val	Ile	Tyr	Arg	Ala	Thr	Thr	Gln	Trp	
385					390					395					400	
Phe	Ile	Leu	Met	Asp	Glu	Pro	Phe	Ile	Gln	Asn	Asp	Gly	Ser	Gln	Lys	
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Thr	Leu	Arg	Glu	Val	Ala	Leu	Asp	Ala	Ile	Glu	Lys	Val	Glu	Phe	Val	
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Pro	Ser	Ser	Gly	Lys	Asn	Arg	Leu	Lys	Thr	Met	Ile	Glu	Asn	Arg	Pro	
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Phe	Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	
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Glu	His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	
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Glu	Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	
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Lys	His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	
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Gln	Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	
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Trp	Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	
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Pro	Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	
			580					585					590			
Glu	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	
	595						600					605				
Leu	Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn	
610						615					620					
Asp	Tyr	Gln	Asn	Asp	Leu	Arg	Val	Ser	Gln	Thr	Phe	Phe	Thr	Gln	Thr	
625					630					635					640	
Glu	Gln	His	Tyr	Lys	Lys	Phe	Arg	Asn	Thr	Leu	Lys	Phe	Leu	Leu	Ala	
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Asn	Phe	Ser	Asp	Met	Asp	Leu	Lys	Asn	Leu	Glu	Arg	Pro	His	Asn	Phe	
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Ser	Pro	Leu	Asp	His	Phe	Met	Leu	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Ala	
	675						680					685				
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690						695					700					
Ile	Leu	Met	Ala	Phe	Val	Thr	Asn	Glu	Leu	Ser	Gly	Ile	Tyr	Leu	Asp	
705					710					715					720	
Ala	Cys	Lys	Asp	Ser	Leu	Tyr	Cys	Asp	Ser	Lys	Asn	Asn	Glu	Lys	Arg	
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Gln	Ala	Ile	Gln	Met	Val	Leu	Leu	Ala	Thr	Ala	Ser	Lys	Leu	Cys	Tyr	
			740					745					750			
Phe	Leu	Ala	Pro	Ile	Leu	Thr	His	Thr	Ile	Glu	Glu	Val	Leu	Glu	His	
	755						760					765				
Ser	Gln	Ala	Leu	Arg	Ile	Phe	Leu	Gln	Ala	Lys	Asp	Val	Phe	Asp	Leu	
770						775					780					
Lys	Asp	Ile	Ser	Val	Ser	Glu	Lys	Leu	His	Leu	Lys	Glu	Phe	Lys	Lys	
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Pro	Glu	Asn	Phe	Glu	Ala	Val	Leu	Ala	Leu	Arg	Ser	Ala	Phe	Asn	Glu	

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Cys	Ala	Ile	Glu	Val	Lys	Glu	Lys	Ala	Leu	Asp	Glu	Asn	Leu	Val	Glu				
		835					840					845							
Glu	Leu	Leu	Met	Val	Ser	Phe	Val	Gly	Ile	Ala	Lys	Glu	Lys	Leu	Ser				
	850					855					860								
Glu	Thr	Pro	Ala	Phe	Thr	Leu	Phe	Lys	Ala	Pro	Phe	Tyr	Lys	Cys	Pro				
865					870					875					880				
Arg	Cys	Trp	Arg	Phe	Lys	Ser	Glu	Leu	Glu	Asn	Thr	Pro	Cys	Lys	Arg				
			885					890					895						
Cys	Glu	Gln	Val	Leu	Lys	Glu	Arg												
			900																

<210> 159
 <211> 339
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (70)...(288)

<400> 159
 tgtagaatga aatcctagcc agtgagctag aatttaaatt tttaatcaaa ggagtcacatca 60
 tggcacacc atg aag aac aac acg gcg ggc acc acc acc acc atc acc aca 111
 Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr
 1 5 10

cac acc acc acc act atc atg gcg gtg aac acc acc atc acc acc aca 159
 His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr
 15 20 25 30

gct ctc atc atg aag aag gtt gtt gca gca cta gcg aca gtc atc atc 207
 Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile
 35 40 45

aag aag aag gtt gct gcc acg ggc atc acg agt aat atc ggt gtg gct 255
 Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala
 50 55 60

agg ggc aac ttg act agg gtt gtc tct ggc ttt tgactttaaa atacaatcat 308
 Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe
 65 70

tccattctaa cccattctga tcaaaccggt t 339

<210> 160
 <211> 73
 <212> PRT
 <213> Helicobacter pylori

<400> 160
 Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

1	5	10	15
Thr Thr Thr	Ile Met Ala Val Asn Thr	Thr Thr Ile Thr Thr Thr	Ala Leu
	20	25	30
Ile Met Lys	Lys Val Val Ala Ala Leu	Ala Thr Val Ile Ile Lys Lys	
	35	40	45
Lys Val Ala	Ala Thr Gly Ile Thr Ser Asn	Ile Gly Val Ala Arg Gly	
	50	55	60
Asn Leu Thr	Arg Val Val Ser Gly Phe		
65	70		

<210> 161
 <211> 787
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(734)

<400> 161
 gttttctact tatgatttttg tggaagaata ttgcaaatta aaggaaatgc atg ctt 56
Met Leu
1

gaa aaa gtg ttt caa gaa att acc aat aaa aga aag ttt ttt gca agt 104
 Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe Ala Ser
5 10 15

tct agc aca ggg gag cag ttt gaa aac caa ttt agg aat gaa tta aaa 152
 Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu Leu Lys
20 25 30

aaa cac ttt agc gaa atc aat ggc gat tta aca gaa gaa tta agc cat 200
 Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu Ser His
35 40 45 50

att gaa gaa aag cct aat aaa gaa atc aaa acc act ttt aac caa ctc 248
 Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn Gln Leu
55 60 65

aaa aag caa gtt tta gaa aaa aat cac ccg cac acc ctt aaa aac cct 296
 Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys Asn Pro
70 75 80

ttt tca aac ctt aca agc cat ttt tta tac cag cct ttt ggc tca caa 344
 Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly Ser Gln
85 90 95

aat tac cct gat ttt ttg gtt ttt att ttt gac tat gtg gtg ggg att 392
 Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val Gly Ile
100 105 110

gaa atc aag ttt tct aaa aac gat aag ggt gaa aaa aat ctt caa aca 440
 Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu Gln Thr

115	120	125	130	
tct cgc ccc atg tgg aat tca aac ctg cct aaa ccc aat gcg att tat	488			
Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala Ile Tyr				
135 140 145				
gtg tat gga gtc gct aat gca aac atc act ttt ttt aaa ggc tca gat	536			
Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly Ser Asp				
150 155 160				
att ttg agt tat gaa acc aga gag gtc ttg ctc aag tat ttt gat att	584			
Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe Asp Ile				
165 170 175				
tta gat aaa gat gaa aga agt ttg aaa aac gcc tta aag gat tta gaa	632			
Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp Leu Glu				
180 185 190				
aac cct ttt ggg ttt gcc ccc tac atc aga aaa gct tat gag cat aaa	680			
Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys				
195 200 205 210				
agg aat ttt cta acc acc acc aga ttg aaa gct tct ttt cgc cca acc	728			
Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr				
215 220 225				
aca ttt taagagagcg gaatgtcttg gaatttttga aaacgctcac tcattagcgt	784			
Thr Phe				
att	787			
<210> 162				
<211> 228				
<212> PRT				
<213> Helicobacter pylori				
<400> 162				
Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe				
1 5 10 15				
Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu				
20 25 30				
Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu				
35 40 45				
Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn				
50 55 60				
Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys				
65 70 75 80				
Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly				
85 90 95				
Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val				
100 105 110				
Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu				
115 120 125				
Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala				

130	135	140
Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly		
145	150	155
Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe		
	165	170
Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp		
	180	185
Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu		
	195	200
His Lys Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg		
	210	220
Pro Thr Thr Phe		
225		

<210> 163
 <211> 540
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (53)...(493)

<400> 163
 ccaaaccctt ttgaaacact tgctcactaa cccattataa gccgcaaaaa cc atg ctc 58
Met Leu
1

tct tta aaa caa gat tcc ttt ttt ttc tta tgt tta gga atc ctg ggg	106
Ser Leu Lys Gln Asp Ser Phe Phe Leu Cys Leu Gly Ile Leu Gly	
5 10 15	

ttt tat ttt tat agc ctt ttg agg gat tta atg cct ttt tta ccc cca	154
Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu Pro Pro	
20 25 30	

atg att ggg ttt tta ttc ttg ttt tat gcg aaa aaa tac gat cat ttt	202
Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp His Phe	
35 40 45 50	

tta ccc agt ttg agc gtg ttt ggt tgt ttg ttt tgg ttt gag agc atg	250
Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu Ser Met	
55 60 65	

cat tta aag act tta ggc gtt tta gct tta ttg ttt tta atc tac cat	298
His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile Tyr His	
70 75 80	

caa atc gcc tat aaa aac tct tta aag ctt ttt aat gac ggc ttt tta	346
Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly Phe Leu	
85 90 95	

ttc aaa act ttg cat gtt ttt ttg gtt tat tac ctt tat tta tcg cgc	394
Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu Ser Arg	

100	105	110	
ttt ttt tcg atg tct ttg agt ttg aaa ata ctc ggc ttt ctc gct ctt			442
Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu Ala Leu			
115	120	125	130
ttt gct tta ata gaa agc gct ttg tgg ggt ttg tat gaa aaa tct tcg			490
Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys Ser Ser			
	135	140	145
cta taagcttttg ctctttgttt ttataggggtt ttgggggtta ctagcct			540
Leu			

<210> 164
 <211> 147
 <212> PRT
 <213> Helicobacter pylori

<400> 164

Met Leu Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile			
1	5	10	15
Leu Gly Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu			
	20	25	30
Pro Pro Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp			
	35	40	45
His Phe Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu			
	50	55	60
Ser Met His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile			
65	70	75	80
Tyr His Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly			
	85	90	95
Phe Leu Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu			
	100	105	110
Ser Arg Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu			
	115	120	125
Ala Leu Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys			
	130	135	140
Ser Ser Leu			
145			

<210> 165
 <211> 1888
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1835)

<400> 165

cactaaagtc aatccaagcg caagttggat gaaaaaataa gaaggaagtt atg aaa	56
	Met Lys

aag tca ttc aaa aaa tta ggc ttt gtc tct tta gcg gct agt ggc gtg	104
Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser Gly Val	
5 10 15	
ctt tta ggg agc atg aac gct acc gat tta gaa acc tac gca gca ttg	152
Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala Ala Leu	
20 25 30	
caa aaa tca tcg cat gtt ttt ggt aat tat gct gaa aag gat aag gat	200
Gln Lys Ser Ser His Val Phe Gly Asn Tyr Ala Glu Lys Asp Lys Asp	
35 40 45 50	
agt aaa tta aca agc gat tca cca acg caa caa caa gat caa aaa gta	248
Ser Lys Leu Thr Ser Asp Ser Pro Thr Gln Gln Gln Asp Gln Lys Val	
55 60 65	
gcc caa aac acc gct tca aac gac agc caa gaa gcg aca aca ctt gaa	296
Ala Gln Asn Thr Ala Ser Asn Asp Ser Gln Glu Ala Thr Thr Leu Glu	
70 75 80	
aac acc gct tct act gac aac aca acc gcc aca act gat gaa act tat	344
Asn Thr Ala Ser Thr Asp Asn Thr Thr Ala Thr Thr Asp Glu Thr Tyr	
85 90 95	
aca aaa agc act gac act act gta gct ggt gcg gct caa aaa gta gaa	392
Thr Lys Ser Thr Asp Thr Thr Val Ala Gly Ala Ala Gln Lys Val Glu	
100 105 110	
acc gat aac aca gcc gtt caa agc gct gaa caa act tta aaa aca gat	440
Thr Asp Asn Thr Ala Val Gln Ser Ala Glu Gln Thr Leu Lys Thr Asp	
115 120 125 130	
gta gct aaa gtt caa gct gat gct agt gct aaa gat ttt gat gaa acc	488
Val Ala Lys Val Gln Ala Asp Ala Ser Ala Lys Asp Phe Asp Glu Thr	
135 140 145	
act ttt caa gcc gat caa gca gca gag caa acc gct gaa aaa gct tta	536
Thr Phe Gln Ala Asp Gln Ala Ala Glu Gln Thr Ala Glu Lys Ala Leu	
150 155 160	
caa cag gct gag agc aaa ctc aac acc gat caa cag act tta aac aca	584
Gln Gln Ala Glu Ser Lys Leu Asn Thr Asp Gln Gln Thr Leu Asn Thr	
165 170 175	
gcg tta caa gat cag acg aaa aca cca acc cca tca acc cca cca act	632
Ala Leu Gln Asp Gln Thr Lys Thr Pro Thr Pro Ser Thr Pro Pro Thr	
180 185 190	
aaa gag gaa cca aaa cac acc gct tca agc ggc aca cca cca gct cca	680
Lys Glu Glu Pro Lys His Thr Ala Ser Ser Gly Thr Pro Pro Ala Pro	
195 200 205 210	
gaa agc cca cca gct aaa aaa gat gaa aca agt ggc aca cca agt gct	728

Glu	Ser	Pro	Pro	Ala	Lys	Lys	Asp	Glu	Thr	Ser	Gly	Thr	Pro	Ser	Ala	
				215					220					225		
agt	ggg	agt	tct	gtg	gca	agc	cag	cta	acc	aaa	gat	acc	act	atg	gtt	776
Ser	Gly	Ser	Ser	Val	Ala	Ser	Gln	Leu	Thr	Lys	Asp	Thr	Thr	Met	Val	
			230					235					240			
aat	aat	ctt	aag	agt	gtg	agc	gtg	agc	gcg	atg	aac	acc	act	tta	agt	824
Asn	Asn	Leu	Lys	Ser	Val	Ser	Val	Ser	Ala	Met	Asn	Thr	Thr	Leu	Ser	
		245					250					255				
gga	gta	gaa	acc	atg	tct	caa	caa	act	gca	acg	att	ggc	aac	ctt	ttg	872
Gly	Val	Glu	Thr	Met	Ser	Gln	Gln	Thr	Ala	Thr	Ile	Gly	Asn	Leu	Leu	
	260					265					270					
aat	agt	agc	acc	gat	tta	agc	agt	gtg	att	ccc	aac	gct	caa	ggg	cta	920
Asn	Ser	Ser	Thr	Asp	Leu	Ser	Ser	Val	Ile	Pro	Asn	Ala	Gln	Gly	Leu	
	275				280					285					290	
aac	agc	gcg	ttt	agc	aca	tta	gaa	agc	gct	caa	aac	act	cta	aaa	ggc	968
Asn	Ser	Ala	Phe	Ser	Thr	Leu	Glu	Ser	Ala	Gln	Asn	Thr	Leu	Lys	Gly	
			295						300					305		
tat	tta	aat	tct	tct	agc	gcg	acg	att	ggg	caa	ttg	aca	aac	gga	tct	1016
Tyr	Leu	Asn	Ser	Ser	Ser	Ala	Thr	Ile	Gly	Gln	Leu	Thr	Asn	Gly	Ser	
			310					315					320			
aat	gcg	gtt	gtg	ggc	gcg	tta	gat	aaa	gct	atc	aat	caa	gtg	gat	atg	1064
Asn	Ala	Val	Val	Gly	Ala	Leu	Asp	Lys	Ala	Ile	Asn	Gln	Val	Asp	Met	
		325					330					335				
gct	ttg	gcc	gat	ctt	agt	gca	gct	gat	acg	caa	aaa	acg	caa	gcc	gtt	1112
Ala	Leu	Ala	Asp	Leu	Ser	Ala	Ala	Asp	Thr	Gln	Lys	Thr	Gln	Ala	Val	
	340					345					350					
acg	ctt	gca	act	gct	agt	gat	agt	cca	acg	aca	acg	aca	gat	gcc	atc	1160
Thr	Leu	Ala	Thr	Ala	Ser	Asp	Ser	Pro	Thr	Thr	Thr	Thr	Asp	Ala	Ile	
	355				360				365						370	
aat	ttc	tta	aac	gcg	cta	aaa	agc	aat	cta	atg	gct	caa	aaa	gac	gct	1208
Asn	Phe	Leu	Asn	Ala	Leu	Lys	Ser	Asn	Leu	Met	Ala	Gln	Lys	Asp	Ala	
				375					380					385		
ttt	ttg	aat	gtg	cat	aaa	aac	att	caa	acc	gct	gtc	gct	caa	gcc	cag	1256
Phe	Leu	Asn	Val	His	Lys	Asn	Ile	Gln	Thr	Ala	Val	Ala	Gln	Ala	Gln	
			390					395					400			
gaa	acc	tac	acg	cca	agc	gtg	atc	aac	acc	aat	aat	tac	ggg	caa	atg	1304
Glu	Thr	Tyr	Thr	Pro	Ser	Val	Ile	Asn	Thr	Asn	Asn	Tyr	Gly	Gln	Met	
		405					410					415				
tat	ggg	gta	gat	gcg	atg	gca	ggg	tat	aag	tgg	ttc	ttt	ggc	aaa	acc	1352
Tyr	Gly	Val	Asp	Ala	Met	Ala	Gly	Tyr	Lys	Trp	Phe	Phe	Gly	Lys	Thr	
	420					425					430					

aaa cgc ttt ggc ttt agg tct tat gga tac tac agc tat aac cat gcg	1400
Lys Arg Phe Gly Phe Arg Ser Tyr Gly Tyr Tyr Ser Tyr Asn His Ala	
435 440 445 450	
aat tta agc ttt gtg ggg agc cag ctt gga atc atg gag ggc gcg tct	1448
Asn Leu Ser Phe Val Gly Ser Gln Leu Gly Ile Met Glu Gly Ala Ser	
455 460 465	
caa gtg aat aac ttc act tat ggc gtg ggc ttt gat gtg ctc tat aac	1496
Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu Tyr Asn	
470 475 480	
ttc tat gaa agc aaa gag ggc tat aac aca gca ggg ttg ttc tta ggc	1544
Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe Leu Gly	
485 490 495	
ttt ggg tta gga ggg gat tgc ttt atc gtt caa gga gag agc tac ttg	1592
Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser Tyr Leu	
500 505 510	
aaa tct caa atg cac att tgc aac aac acc gcc ggc tgt tca gcg agc	1640
Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser Ala Ser	
515 520 525 530	
atg aac aca agc tac ttc caa atg cct gtt gaa ttt ggt ttt agg agc	1688
Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe Arg Ser	
535 540 545	
aat ttc tct aaa cac agc ggg att gaa gtg ggc ttt aaa ttg cct tta	1736
Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu Pro Leu	
550 555 560	
ttc acc aac caa ttc tat aaa gaa agg ggc gta gat gga tgc gta gat	1784
Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser Val Asp	
565 570 575	
gtg ttc tat aaa agg aat ttc tct att tat ttt aac tac atg atc aac	1832
Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn	
580 585 590	
ttc taagcctttc tattctttcc aatagagggt tttctctctg ttggtttctt	1885
Phe	
595	
ttt	1888
<210> 166	
<211> 595	
<212> PRT	
<213> Helicobacter pylori	
<400> 166	
Met Lys Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser	
1 5 10 15	
Gly Val Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala	

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Ala Ser Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu
465 470 475 480
Tyr Asn Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe
485 490 495
Leu Gly Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser
500 505 510
Tyr Leu Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser
515 520 525
Ala Ser Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe
530 535 540
Arg Ser Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu
545 550 555 560
Pro Leu Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser
565 570 575
Val Asp Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met
580 585 590
Ile Asn Phe
595

<210> 167
<211> 1467
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (46)...(1416)

<400> 167
tttaagaaac tatttgcgca tttgatgtta aggtttctct aaagc atg cgt tat ttt 57
Met Arg Tyr Phe
1

ctt gta gtt ttc ttg ttt ttg ttt gtg ggt tgc aca aaa aag gat ttc 105
Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr Lys Lys Asp Phe
5 10 15 20

acg ctc aaa gat tta tcc ttg ccc caa gag gct tca agc tat ctt gca 153
Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser Ser Tyr Leu Ala
25 30 35

tct caa aat ggc agt aac aac aac caa agc att gac ccc caa gcg tta 201
Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile Asp Pro Gln Ala Leu
40 45 50

aga gaa aat ctg aaa gag agc tat ctc aaa gcg tgg tat tcc cca tgg 249
Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala Trp Tyr Ser Pro Trp
55 60 65

cta gat atg aaa gtc aaa agc aat aaa aaa gaa gtg ttt tgg atc ctt 297
Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu Val Phe Trp Ile Leu
70 75 80

aag gag atg aat aaa tcc acc ggt tat ggc gaa gat cta aaa ccc aac 345

Lys	Glu	Met	Asn	Lys	Ser	Thr	Gly	Tyr	Gly	Glu	Asp	Leu	Lys	Pro	Asn		
85					90					95					100		
gca	aaa	gct	ttc	aat	gac	gca	ctc	att	aag	agc	atg	gat	att	gag	cat	393	
Ala	Lys	Ala	Phe	Asn	Asp	Ala	Leu	Ile	Lys	Ser	Met	Asp	Ile	Glu	His		
				105					110					115			
tac	cct	agc	gtt	aag	att	agg	gct	gtt	gta	gcg	cga	gat	agc	gat	gtg	441	
Tyr	Pro	Ser	Val	Lys	Ile	Arg	Ala	Val	Val	Ala	Arg	Asp	Ser	Asp	Val		
			120					125					130				
agg	gct	gtg	cct	act	aac	aaa	cct	tat	tat	ctt	tct	caa	aaa	ggc	tat	489	
Arg	Ala	Val	Pro	Thr	Asn	Lys	Pro	Tyr	Tyr	Leu	Ser	Gln	Lys	Gly	Tyr		
			135				140					145					
cct	ttt	gat	agg	tat	caa	aat	tcg	ctg	att	ttt	caa	ggc	acg	ccg	gtt	537	
Pro	Phe	Asp	Arg	Tyr	Gln	Asn	Ser	Leu	Ile	Phe	Gln	Gly	Thr	Pro	Val		
	150					155					160						
tta	atc	acg	cat	ttt	aat	cta	gat	aaa	act	tat	gcc	cac	att	caa	agc	585	
Leu	Ile	Thr	His	Phe	Asn	Leu	Asp	Lys	Thr	Tyr	Ala	His	Ile	Gln	Ser		
165					170					175					180		
agt	ttt	gtt	tat	ggc	tgg	atc	aaa	gtt	agc	gat	tta	gtc	tac	atg	cac	633	
Ser	Phe	Val	Tyr	Gly	Trp	Ile	Lys	Val	Ser	Asp	Leu	Val	Tyr	Met	His		
				185				190						195			
gat	aaa	gac	ata	gag	ctt	tta	acc	cat	ctt	aaa	gat	tat	gtc	atg	cct	681	
Asp	Lys	Asp	Ile	Glu	Leu	Leu	Thr	His	Leu	Lys	Asp	Tyr	Val	Met	Pro		
			200					205					210				
ata	aaa	gat	aaa	atc	ccc	ctt	tat	aca	gac	tat	ggg	gat	ttt	tac	acc	729	
Ile	Lys	Asp	Lys	Ile	Pro	Leu	Tyr	Thr	Asp	Tyr	Gly	Asp	Phe	Tyr	Thr		
		215					220					225					
aac	gcc	aga	gtg	ggc	gaa	ttg	ttc	gct	ctc	atc	ccc	caa	agt	caa	aaa	777	
Asn	Ala	Arg	Val	Gly	Glu	Leu	Phe	Ala	Leu	Ile	Pro	Gln	Ser	Gln	Lys		
	230					235					240						
aca	cct	caa	aaa	ccc	caa	aaa	aag	gaa	ttg	aaa	gcc	tat	ggc	ttt	ttg	825	
Thr	Pro	Gln	Lys	Pro	Gln	Lys	Lys	Glu	Leu	Lys	Ala	Tyr	Gly	Phe	Leu		
245					250					255					260		
aga	gac	gct	aag	ggc	tat	gca	gct	tta	caa	agc	gtg	atc	tta	gaa	gaa	873	
Arg	Asp	Ala	Lys	Gly	Tyr	Ala	Ala	Leu	Gln	Ser	Val	Ile	Leu	Glu	Glu		
				265				270						275			
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Lys	Asp	Phe	Phe	Val	Phe	Pro	Lys	Ala	Phe	Asn	Ser	Glu	Asn	Met	Ala		
			280					285					290				
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Tyr	Phe	Ile	Asp	Thr	Met	Leu	Gly	Gln	Lys	Tyr	Gly	Trp	Gly	Gly	Leu		
		295					300					305					

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Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala Asn	
310 315 320	
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Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr Ala	
325 330 335 340	
aac aat tat gtg gat tta agc tct atg aaa gcc aaa gaa aaa gaa gac	1113
Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu Asp	
345 350 355	
tac atc ctt aaa aac gcc acg cct ttt gga acg ctc atc tat tta aaa	1161
Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu Lys	
360 365 370	
ggg cat atc atg ctt tat tta ggc gca cac aac cat caa gcg ata gtc	1209
Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile Val	
375 380 385	
gct cac agc att tgg tcg gtg caa acc caa aag cat ttt aaa acc ttg	1257
Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr Leu	
390 395 400	
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Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala Glu	
405 410 415 420	
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Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg Val	
425 430 435	
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Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser Pro	
440 445 450	
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<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 168

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Ser Tyr Leu Ala Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile
35 40 45
Asp Pro Gln Ala Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala

50					55					60					
Trp	Tyr	Ser	Pro	Trp	Leu	Asp	Met	Lys	Val	Lys	Ser	Asn	Lys	Lys	Glu
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	130					135					140				
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Gln	Gly	Thr	Pro	Val	Leu	Ile	Thr	His	Phe	Asn	Leu	Asp	Lys	Thr	Tyr
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Ala	His	Ile	Gln	Ser	Ser	Phe	Val	Tyr	Gly	Trp	Ile	Lys	Val	Ser	Asp
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225					230					235					240
Pro	Gln	Ser	Gln	Lys	Thr	Pro	Gln	Lys	Pro	Gln	Lys	Lys	Glu	Leu	Lys
			245						250					255	
Ala	Tyr	Gly	Phe	Leu	Arg	Asp	Ala	Lys	Gly	Tyr	Ala	Ala	Leu	Gln	Ser
		260					265						270		
Val	Ile	Leu	Glu	Glu	Lys	Asp	Phe	Phe	Val	Phe	Pro	Lys	Ala	Phe	Asn
	275						280					285			
Ser	Glu	Asn	Met	Ala	Tyr	Phe	Ile	Asp	Thr	Met	Leu	Gly	Gln	Lys	Tyr
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Asp	Ser	Phe	Ala	Asn	Phe	Gly	Ile	Leu	Leu	Pro	Arg	Asn	Ser	Tyr	Ala
			325						330					335	
Gln	Ser	Arg	Tyr	Ala	Asn	Asn	Tyr	Val	Asp	Leu	Ser	Ser	Met	Lys	Ala
		340					345						350		
Lys	Glu	Lys	Glu	Asp	Tyr	Ile	Leu	Lys	Asn	Ala	Thr	Pro	Phe	Gly	Thr
	355						360					365			
Leu	Ile	Tyr	Leu	Lys	Gly	His	Ile	Met	Leu	Tyr	Leu	Gly	Ala	His	Asn
	370				375					380					
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385				390						395					400
His	Phe	Lys	Thr	Leu	Ser	His	Lys	Ile	Gly	Gly	Val	Val	Ile	Thr	Ser
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Leu	Trp	Leu	Ala	Glu	Glu	His	Asn	Gly	Ala	Phe	Ser	Lys	Lys	Lys	Leu
	420						425						430		
Leu	Ile	Asp	Arg	Val	Leu	Gly	Met	Ser	Asp	Leu	Lys	Asp	Phe	Val	Asn
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<211> 235

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Glu	Tyr	Lys	Arg	Gln	Asn	Glu	His	Leu	Glu	Met	Ile	Ala	Ser	Glu	Asn	
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tac	act	ttt	gca	agc	gtt	atg	gag	gct	atg	ggg	agt	gtt	tta	acg	aat	200
Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu	Thr	Asn	
	35				40				45					50		
aaa	tac	gct	gaa	ggc	tac	cct	aac	aag	cgc	tat	tat	gga	ggc	tgt	gaa	248
Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly	Cys	Glu	
				55				60						65		
gtg	gtg	gat	aaa	ata	gaa	agc	cta	gcc	ata	gaa	agg	gct	aaa	aag	ctt	296
Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys	Lys	Leu	
			70					75					80			
ttt	aat	tgc	cag	ttc	gct	aac	gtg	caa	gcg	cat	tca	ggc	tca	caa	gcc	344
Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser	Gln	Ala	
	85					90						95				
aat	aac	gct	gtc	tat	cac	gct	ctt	tta	aag	cct	tat	gac	aag	att	tta	392
Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys	Ile	Leu	
	100					105					110					
ggc	atg	gat	tta	agc	tgt	gga	ggg	cat	tta	acg	cat	ggc	gct	aaa	gtg	440
Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala	Lys	Val	
	115				120					125				130		
agt	tta	acc	ggc	aag	cat	tat	cag	agc	ttt	tct	tat	ggc	gtg	aat	ttg	488
Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val	Asn	Leu	
			135					140						145		
gat	ggc	tat	att	gat	tat	gaa	gag	gcg	cta	aaa	atc	gct	caa	agc	gtt	536
Asp	Gly	Tyr	Ile	Asp	Tyr	Glu	Glu	Ala	Leu	Lys	Ile	Ala	Gln	Ser	Val	
			150					155					160			
aag	cca	gaa	atc	atc	gtg	tgc	ggg	ttt	tca	gcc	tat	cca	agg	gag	att	584
Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg	Glu	Ile	
		165					170					175				
gat	ttt	aag	aaa	ttt	aga	gaa	atc	gct	gat	gaa	gtg	ggg	gcg	tta	cta	632
Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	Leu	Leu	
	180					185					190					
tta	ggc	gat	ata	gcc	cat	gtg	gca	ggg	ctt	gtg	gta	acc	ggt	gag	cat	680
Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	Glu	His	
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gcc	cat	cct	ttc	ccg	cat	tgc	cat	gtg	gtt	tca	agc	acc	act	cat	aag	728
Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	His	Lys	
				215					220					225		

acc tta aga ggg cct aga ggg ggg att att tta act aat gat gaa gag	776
Thr Leu Arg Gly Pro Arg Gly Gly Ile Ile Leu Thr Asn Asp Glu Glu	
230 235 240	
ata gcg gct aag att gac aaa gcg att ttt cca gga act caa ggc ggg	824
Ile Ala Ala Lys Ile Asp Lys Ala Ile Phe Pro Gly Thr Gln Gly Gly	
245 250 255	
cct ttg atg cat gtg att gct gct aaa gcg gtg ggt ttt aaa gag aat	872
Pro Leu Met His Val Ile Ala Ala Lys Ala Val Gly Phe Lys Glu Asn	
260 265 270	
cta aaa cca gaa ttt aaa gct tat gca caa tta gtg aaa tct aac atg	920
Leu Lys Pro Glu Phe Lys Ala Tyr Ala Gln Leu Val Lys Ser Asn Met	
275 280 285 290	
caa gtt ttg gct aaa gcg tta aaa gaa aaa aac cat aag tta gtg agt	968
Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu Val Ser	
295 300 305	
ggg ggc act tct aac cat ttg ctt tta atg gat ttt tta gat aag cct	1016
Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp Lys Pro	
310 315 320	
tat agc ggg aaa gac gct gat att gca tta ggg aat gcc gga atc acc	1064
Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly Ile Thr	
325 330 335	
gtg aat aaa aac acc att cct ggt gaa acg cgc agc cct ttt gta acg	1112
Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe Val Thr	
340 345 350	
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Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly Met Gly	
355 360 365 370	
gct aag gaa ttt gaa atc ata ggg aat aaa ata tca gat att ttg aat	1208
Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile Leu Asn	
375 380 385	
gat att aat aat gtt agt ttg caa ttg cat gtg aaa gaa gaa ttg aaa	1256
Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu Leu Lys	
390 395 400	
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Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe	
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<212> PRT	
<213> Helicobacter pylori	

<400> 172

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Glu	Asn	Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu
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Thr	Asn	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly
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Cys	Glu	Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys
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Lys	Leu	Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser
			85						90					95	
Gln	Ala	Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys
			100						105					110	
Ile	Leu	Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala
			115					120					125		
Lys	Val	Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val
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Ser	Val	Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg
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Glu	Ile	Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala
			180					185					190		
Leu	Leu	Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly
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Glu	His	Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr
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His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Ile	Leu	Thr	Asn	Asp
225					230					235					240
Glu	Glu	Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln
			245						250					255	
Gly	Gly	Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys
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Glu	Asn	Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser
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Asn	Met	Gln	Val	Leu	Ala	Lys	Ala	Leu	Lys	Glu	Lys	Asn	His	Lys	Leu
			290				295					300			
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305					310					315					320
Lys	Pro	Tyr	Ser	Gly	Lys	Asp	Ala	Asp	Ile	Ala	Leu	Gly	Asn	Ala	Gly
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Ile	Thr	Val	Asn	Lys	Asn	Thr	Ile	Pro	Gly	Glu	Thr	Arg	Ser	Pro	Phe
			340					345					350		
Val	Thr	Ser	Gly	Ile	Arg	Ile	Gly	Ser	Ala	Ala	Leu	Ser	Ala	Arg	Gly
			355				360					365			
Met	Gly	Ala	Lys	Glu	Phe	Glu	Ile	Ile	Gly	Asn	Lys	Ile	Ser	Asp	Ile
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Leu	Asn	Asp	Ile	Asn	Asn	Val	Ser	Leu	Gln	Leu	His	Val	Lys	Glu	Glu
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Leu	Lys	Ala	Met	Val	Asn	Gln	Phe	Pro	Val	Tyr	His	Gln	Pro	Ile	Phe
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<211> 1513
<212> DNA
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<400> 173

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35 40 45 50

gca act ctt ttg cgt gaa agc ctg aaa aac aat gca caa cca tca caa 296
Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro Ser Gln
70 75 80

gcc aat tta gag caa tct cta ggg att tta gga aaa cta ttg gat cta 392
Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu Asp Leu
100 105 110

gtg ggg aaa gaa caa atc ggt atc acg gat agc atg ctc ttg gtg gct 488
Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu Val Ala
135 140 145

caa aac aat aac gaa cag cta tac gaa aat att atg aaa gtc atg ctt 584

Gln	Asn	Asn	Asn	Glu	Gln	Leu	Tyr	Glu	Asn	Ile	Met	Lys	Val	Met	Leu		
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Leu	Gly	Ala	Gly	Gly	Thr	Asn	Gly	Ala	Tyr	Asn	Gly	Val	Ser	Val	Gly		
	180					185					190						
gac	att	gcc	acg	ggc	atg	caa	aat	ttt	tct	tcg	caa	acg	ggc	ttg	ata	680	
Asp	Ile	Ala	Thr	Gly	Met	Gln	Asn	Phe	Ser	Ser	Gln	Thr	Gly	Leu	Ile		
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Gly	Ala	Asn	Ser	Thr	Val	Ser	Glu	Leu	Asn	Ala	Leu	Ile	Lys	Ser	Gly		
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att	tct	ttg	gat	cgt	gag	act	ttg	ggg	tta	ggg	agt	ttt	att	gaa	aaa	776	
Ile	Ser	Leu	Asp	Arg	Glu	Thr	Leu	Gly	Leu	Gly	Ser	Phe	Ile	Glu	Lys		
			230					235					240				
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Asn	Ile	Cys	Ser	Gly	Ala	Ser	Ser	Cys	Phe	Ser	Gly	Asn	Gln	Leu	Ile		
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Tyr	Lys	Lys	Gly	Leu	Asp	Arg	Thr	Ile	Asn	Ile	Ile	Asn	Thr	Val	Leu		
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Gly	Gln	Phe	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Tyr	Ile		
	275				280					285					290		
cct	aac	ctc	ttt	tcg	ctc	aag	gat	tac	cag	tca	gcg	agc	atg	aac	ggc	968	
Pro	Asn	Leu	Phe	Ser	Leu	Lys	Asp	Tyr	Gln	Ser	Ala	Ser	Met	Asn	Gly		
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Phe	Gly	Ala	Lys	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Thr	His	Lys	Lys	Asn		
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gtt	ggc	tta	agg	tat	tac	ggg	ttt	ttg	gat	tat	ggc	tat	gcg	aac	ttt	1064	
Val	Gly	Leu	Arg	Tyr	Tyr	Gly	Phe	Leu	Asp	Tyr	Gly	Tyr	Ala	Asn	Phe		
		325				330					335						
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Gly	Thr	Asp	Phe	Leu	Tyr	Asn	Val	Tyr	Glu	Arg	Ser	Arg	Arg	Arg	Glu		
	355				360					365					370		
agg	act	acg	atc	ggc	ctt	ttc	ttt	ggc	gct	caa	att	gca	ggg	caa	act	1208	
Arg	Thr	Thr	Ile	Gly	Leu	Phe	Phe	Gly	Ala	Gln	Ile	Ala	Gly	Gln	Thr		
				375				380						385			

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Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val	
390 395 400	
aag tcc agt tgc ttc caa ttc ttg ttt gat ttg ggc gtg cgc acc aac	1304
Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn	
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ttt gca aaa acc aat ttc aat aag cac agg cta gac caa ggg ata gaa	1352
Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu	
420 425 430	
ttt ggg gtg aaa atc cct gtt atc gct cat aaa tat ttt gca acc caa	1400
Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln	
435 440 445 450	
ggc tca agc gcg agc tat atg agg aat ttt agc ttc tat gtg ggc tat	1448
Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr	
455 460 465	
tca gtc ggt ttt taaggaaggc tcttgatgaa aaataccaat acaaaagaga	1500
Ser Val Gly Phe	
470	

taaagaatac aag	1513
----------------	------

<210> 174
 <211> 470
 <212> PRT
 <213> Helicobacter pylori

<400> 174

Met Ser Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp	
1 5 10 15	
Tyr Gln Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr	
20 25 30	
Gln Ala Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu	
35 40 45	
Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn	
50 55 60	
Lys Thr Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro	
65 70 75 80	
Ser Gln Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln	
85 90 95	
Ala Leu Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu	
100 105 110	
Asp Leu Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val	
115 120 125	
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu	
130 135 140	
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys	
145 150 155 160	
Ile Gln Gln Asn Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val	
165 170 175	
Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser	

5	10	15	
atc atc gtt tat ttt ttc caa gca ttt caa ggg gtt ttg aat ttt gaa			152
Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn Phe Glu			
20	25	30	
ggg ggt ttt tta ggg ttt ttt atc gtg gcg ttg tct tcg tat tac ggc			200
Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr Tyr Gly			
35	40	45	50
gtt aaa aag cgt ttg gat tta agg aaa caa aat tca ata gaa aaa gaa			248
Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu Lys Glu			
55	60	65	
gaa aag caa aaa ttc caa aaa ttc gcc ctg ggc ttg gaa atg tct ttc			296
Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met Ser Phe			
70	75	80	
aat gtg tgg cgt tta gga ggg tat ggg gtt tta cta ggc att tta gga			344
Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile Leu Gly			
85	90	95	
acg ctt tta ttc ttg cat ctt ttt aac ggg tta atc ttt ctt att ggc			392
Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu Ile Gly			
100	105	110	
gtg ttt gtg agc tcg ctc tct agc gcg tta tta cga ttt ttg aat aat			440
Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu Asn Asn			
115	120	125	130
aat ggt aag ttt tgacacaaac tcacatggat ttttaaccctt ttaatcctct			492
Asn Gly Lys Phe			
tttaattttt aat			505
<210> 176			
<211> 134			
<212> PRT			
<213> Helicobacter pylori			
<400> 176			
Met Cys Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val			
1	5	10	15
Ser Ala Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn			
20	25	30	
Phe Glu Gly Gly Phe Leu Gly Phe Ile Val Ala Leu Ser Ser Tyr			
35	40	45	
Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu			
50	55	60	
Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met			
65	70	75	80
Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile			
85	90	95	
Leu Gly Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu			

100 105 110
 Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu
 115 120 125
 Asn Asn Asn Gly Lys Phe
 130

<210> 177
 <211> 511
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(458)

<400> 177
 tttttgcact atcggtgttt gcgctgtggt gtttggcacg cttgaaaaaa atg ctc 56
 Met Leu
 1

 aag agt acc atc aaa gaa gat tat ttg atg ctg atg tct aga gaa gtg 104
 Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val
 5 10 15

 agt gct ttt gtg ggg act ctt ttc ttc att ggc ttg agt tgc tat gcg 152
 Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala
 20 25 30

 atc tat cat ggc aac atg ccc gat tat ttg aga ccg gct ttg ata gac 200
 Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp
 35 40 45 50

 act att aag gca gcg agt gat tcc atc tat tcc agc tgc gac tac atg 248
 Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met
 55 60 65

 gat tat ttt ttg aag gct aga aag atg tta gag ggg ttt gct tgg tgg 296
 Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp
 70 75 80

 agc atg ttc aaa gcg gag agc atg ggc tta aat aag ggg ttt atg gtt 344
 Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val
 85 90 95

 gcg ggc tgg gta gcg ttt atc atc tat aac gct ctt agc ggg ata gcc 392
 Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala
 100 105 110

 atc agc agg ctg agc gct caa atc att tat tgg tta tca aaa tat ttt 440
 Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe
 115 120 125 130

 agg agt gag tat gga aaa tgatgttaaa gaagatctag agcaagcaag 488
 Arg Ser Glu Tyr Gly Lys

accaaagtta gagccagaaa agc

511

<210> 178
 <211> 136
 <212> PRT
 <213> Helicobacter pylori

<400> 178
 Met Leu Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg
 1 5 10 15
 Glu Val Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys
 20 25 30
 Tyr Ala Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu
 35 40 45
 Ile Asp Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp
 50 55 60
 Tyr Met Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala
 65 70 75 80
 Trp Trp Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe
 85 90 95
 Met Val Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly
 100 105 110
 Ile Ala Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys
 115 120 125
 Tyr Phe Arg Ser Glu Tyr Gly Lys
 130 135

<210> 179
 <211> 2203
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(2150)

<400> 179
 gagttacaca ctctttgaga acaaaacgcc aaaccattta ggaaattacc atg cta 56
 Met Leu
 1
 aga ttc gtt agt aaa acg att tgc ttg tct tta atc ggc ttg ttc aac 104
 Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn
 5 10 15
 cct tta gaa gcc ttt caa aaa cac caa aaa gac ggc ttt ttt ata gaa 152
 Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu
 20 25 30
 gct ggg ttt gaa act ggg tta tta gaa gga acg caa act aaa gaa gaa 200
 Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu
 35 40 45 50

gtc ata acc acc caa aaa atc tat gaa aac ccc cta acc cac cca caa	248
Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln	
55 60 65	
act aaa gaa cag cct aaa gaa caa aat aaa agc gat acg gcc acc cca	296
Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro	
70 75 80	
caa agc gct tac gga aaa tac tac ata ccc caa agc acc att tta aaa	344
Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys	
85 90 95	
aat gca acg gct tta ttc acc acg gac aag ata gaa aat ggc tta act	392
Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr	
100 105 110	
ttt tat tct caa aac cct gtg tat gcg aat atg gtt aat ggg agc gta	440
Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val	
115 120 125 130	
acc ata caa aac ttt ctg cct tat aat tta aac aat gtt gaa ctg agt	488
Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser	
135 140 145	
ttt aaa gac gct caa ggc aag gtg gtc aat tta ggc gtg ata gag acc	536
Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr	
150 155 160	
atc cct aaa caa tct caa att acc ttg cct gca agc ttg ttt aat gat	584
Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp	
165 170 175	
tca gaa ttt gaa caa gct gat agc ttt aat tac caa caa ctt caa gcc	632
Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu Gln Ala	
180 185 190	
act gcc aca caa ttt tct gac gct aac acg caa agt ttg ttt caa aag	680
Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe Gln Lys	
195 200 205 210	
ctc agc aag atc aca acc aat gta aca atg agt tat gaa aac gcc gat	728
Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn Ala Asp	
215 220 225	
acc aac aat ttt aaa ggt aat tgc cat gat tgt gtg tca gat ttc acc	776
Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp Phe Thr	
230 235 240	
cca caa acc gca gaa gaa ttg acc aat tta atg cta gat atg att gcg	824
Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met Ile Ala	
245 250 255	
gtg ttt gac tct aaa tcg tgg gaa gaa gcc gtt tta aac gct cct ttc	872
Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala Pro Phe	

260	265	270	
caa ttt tct aac agc tca tca gag tgc ggc tct gac ttt cct aag tgc			920
Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro Lys Cys			
275	280	285	290
gtg aat cct ttc aat aac ggg cgt gtc gct ccc atc tat gaa aaa tac			968
Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu Lys Tyr			
	295	300	305
gtg cta acc cca caa tcc gtt ata gat gcg ttt aga aga acg atc aat			1016
Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr Ile Asn			
	310	315	320
ctt gaa gtg aat atc cta aaa tca ggg ttt gta ggg cta ggg tat gaa			1064
Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly Tyr Glu			
	325	330	335
ctt gat gat aat gat ggt aat ctg ggg ata gaa gct tct gcc tta aat			1112
Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala Leu Asn			
	340	345	350
cct gaa aaa ttg ttt ggt aaa act ttg aac aaa gtt gat att gtg gaa			1160
Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile Val Glu			
	355	360	370
tta aga gac att atc cat gaa ttt agc cac act aaa ggc tat acg cat			1208
Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr Thr His			
	375	380	385
aat ggg aac atg act tat caa aga gtg cgc ttg tgt caa gaa aac ggc			1256
Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu Asn Gly			
	390	395	400
gga gcc ata caa gaa tgt gag ggt ggg aaa gaa gag tta gtc aat gga			1304
Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val Asn Gly			
	405	410	415
aaa gaa gaa cta aaa ttt aca aat ggg aaa gaa gtg aaa gat cag gat			1352
Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp Gln Asp			
	420	425	430
ggt tac acc tat gat gta tgt tct ttt tat aag gac aac cac caa gtc			1400
Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His Gln Val			
	435	440	445
tat aca gcg agc aat tac ccc aat tcc att tat acg aat tgc gct caa			1448
Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln			
	455	460	465
gtc cct gct ggg ctt ata ggg gtt acc acc gct gtc tgg caa cag ctc			1496
Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu			
	470	475	480
atc aat caa aac gct ctg ccc att aat ttc gct aat cta aat agc cca			1544

Ile	Asn	Gln	Asn	Ala	Leu	Pro	Ile	Asn	Phe	Ala	Asn	Leu	Asn	Ser	Pro		
		485						490					495				
acc	aac	cac	tta	aac	gcc	ggg	ttg	aac	gca	caa	aat	ttt	gca	acc	tct	1592	
Thr	Asn	His	Leu	Asn	Ala	Gly	Leu	Asn	Ala	Gln	Asn	Phe	Ala	Thr	Ser		
		500				505						510					
ata	gtc	agc	gcg	atc	gcg	caa	aat	ttt	tcc	acc	act	tcc	acc	acc	act	1640	
Ile	Val	Ser	Ala	Ile	Ala	Gln	Asn	Phe	Ser	Thr	Thr	Ser	Thr	Thr	Thr		
					520					525					530		
tac	cgc	tct	tca	agt	aag	aat	ttt	aga	agc	cct	att	tta	ggg	gtt	aat	1688	
Tyr	Arg	Ser	Ser	Ser	Lys	Asn	Phe	Arg	Ser	Pro	Ile	Leu	Gly	Val	Asn		
				535					540					545			
gtt	aaa	ata	ggc	tac	caa	cat	tat	ttc	aat	gac	tac	ata	ggg	tta	gcc	1736	
Val	Lys	Ile	Gly	Tyr	Gln	His	Tyr	Phe	Asn	Asp	Tyr	Ile	Gly	Leu	Ala		
			550					555					560				
tat	tac	ggc	att	atc	aaa	tac	aat	tac	gcc	aaa	act	aac	gat	gaa	aaa	1784	
Tyr	Tyr	Gly	Ile	Ile	Lys	Tyr	Asn	Tyr	Ala	Lys	Thr	Asn	Asp	Glu	Lys		
		565					570					575					
atc	cag	caa	tta	agc	tat	ggg	ggg	gga	atg	gat	gtg	ttg	ttt	gat	ttc	1832	
Ile	Gln	Gln	Leu	Ser	Tyr	Gly	Gly	Gly	Met	Asp	Val	Leu	Phe	Asp	Phe		
		580				585					590						
atc	acc	act	tac	gct	aac	aaa	aag	caa	gac	aac	cca	act	aaa	aaa	gtt	1880	
Ile	Thr	Thr	Tyr	Ala	Asn	Lys	Lys	Gln	Asp	Asn	Pro	Thr	Lys	Lys	Val		
					600					605					610		
ttt	gct	tcc	tct	ttt	ggg	gtg	ttt	ggg	ggg	tta	agg	ggc	tta	tac	aat	1928	
Phe	Ala	Ser	Ser	Phe	Gly	Val	Phe	Gly	Gly	Leu	Arg	Gly	Leu	Tyr	Asn		
				615					620					625			
agc	tat	tat	gtc	ttc	aac	caa	gtc	aaa	gga	agc	ggg	aat	tta	gat	ata	1976	
Ser	Tyr	Tyr	Val	Phe	Asn	Gln	Val	Lys	Gly	Ser	Gly	Asn	Leu	Asp	Ile		
			630					635					640				
gtt	act	ggg	ttt	aat	tac	cgc	tac	aag	cat	tct	aaa	tat	tct	gta	ggc	2024	
Val	Thr	Gly	Phe	Asn	Tyr	Arg	Tyr	Lys	His	Ser	Lys	Tyr	Ser	Val	Gly		
		645					650					655					
att	agc	gtt	cct	tta	atc	caa	agc	ggg	att	aaa	atc	gct	tct	aat	aat	2072	
Ile	Ser	Val	Pro	Leu	Ile	Gln	Ser	Gly	Ile	Lys	Ile	Ala	Ser	Asn	Asn		
		660				665					670						
ggc	atc	tat	gcg	aac	tcc	gtt	gtt	ttg	aat	gaa	ggg	ggc	agt	cat	ttt	2120	
Gly	Ile	Tyr	Ala	Asn	Ser	Val	Val	Leu	Asn	Glu	Gly	Gly	Ser	His	Phe		
					680					685					690		
aaa	gtg	ttt	ttt	aat	tac	ggg	tgg	att	ttt	taggatttaa	aatccccaat					2170	
Lys	Val	Phe	Phe	Asn	Tyr	Gly	Trp	Ile	Phe								
				695				700									

aaccccctaa acttggtgcga tactcgctac aaa

2203

<210> 180

<211> 700

<212> PRT

<213> Helicobacter pylori

<400> 180

Met	Leu	Arg	Phe	Val	Ser	Lys	Thr	Ile	Cys	Leu	Ser	Leu	Ile	Gly	Leu
1				5					10					15	
Phe	Asn	Pro	Leu	Glu	Ala	Phe	Gln	Lys	His	Gln	Lys	Asp	Gly	Phe	Phe
			20					25					30		
Ile	Glu	Ala	Gly	Phe	Glu	Thr	Gly	Leu	Leu	Glu	Gly	Thr	Gln	Thr	Lys
		35					40					45			
Glu	Glu	Val	Ile	Thr	Thr	Gln	Lys	Ile	Tyr	Glu	Asn	Pro	Leu	Thr	His
	50					55					60				
Pro	Gln	Thr	Lys	Glu	Gln	Pro	Lys	Glu	Gln	Asn	Lys	Ser	Asp	Thr	Ala
65					70					75					80
Thr	Pro	Gln	Ser	Ala	Tyr	Gly	Lys	Tyr	Tyr	Ile	Pro	Gln	Ser	Thr	Ile
			85						90					95	
Leu	Lys	Asn	Ala	Thr	Ala	Leu	Phe	Thr	Thr	Asp	Lys	Ile	Glu	Asn	Gly
			100					105					110		
Leu	Thr	Phe	Tyr	Ser	Gln	Asn	Pro	Val	Tyr	Ala	Asn	Met	Val	Asn	Gly
		115					120					125			
Ser	Val	Thr	Ile	Gln	Asn	Phe	Leu	Pro	Tyr	Asn	Leu	Asn	Asn	Val	Glu
	130					135					140				
Leu	Ser	Phe	Lys	Asp	Ala	Gln	Gly	Lys	Val	Val	Asn	Leu	Gly	Val	Ile
145					150					155					160
Glu	Thr	Ile	Pro	Lys	Gln	Ser	Gln	Ile	Thr	Leu	Pro	Ala	Ser	Leu	Phe
			165						170					175	
Asn	Asp	Ser	Glu	Phe	Glu	Gln	Ala	Asp	Ser	Phe	Asn	Tyr	Gln	Gln	Leu
			180					185					190		
Gln	Ala	Thr	Ala	Thr	Gln	Phe	Ser	Asp	Ala	Asn	Thr	Gln	Ser	Leu	Phe
		195					200					205			
Gln	Lys	Leu	Ser	Lys	Ile	Thr	Thr	Asn	Val	Thr	Met	Ser	Tyr	Glu	Asn
	210					215					220				
Ala	Asp	Thr	Asn	Asn	Phe	Lys	Gly	Asn	Cys	His	Asp	Cys	Val	Ser	Asp
225					230					235					240
Phe	Thr	Pro	Gln	Thr	Ala	Glu	Glu	Leu	Thr	Asn	Leu	Met	Leu	Asp	Met
			245						250					255	
Ile	Ala	Val	Phe	Asp	Ser	Lys	Ser	Trp	Glu	Glu	Ala	Val	Leu	Asn	Ala
		260						265					270		
Pro	Phe	Gln	Phe	Ser	Asn	Ser	Ser	Ser	Glu	Cys	Gly	Ser	Asp	Phe	Pro
		275					280					285			
Lys	Cys	Val	Asn	Pro	Phe	Asn	Asn	Gly	Arg	Val	Ala	Pro	Ile	Tyr	Glu
	290					295					300				
Lys	Tyr	Val	Leu	Thr	Pro	Gln	Ser	Val	Ile	Asp	Ala	Phe	Arg	Arg	Thr
305					310					315					320
Ile	Asn	Leu	Glu	Val	Asn	Ile	Leu	Lys	Ser	Gly	Phe	Val	Gly	Leu	Gly
			325						330					335	
Tyr	Glu	Leu	Asp	Asp	Asn	Asp	Gly	Asn	Leu	Gly	Ile	Glu	Ala	Ser	Ala
		340						345					350		
Leu	Asn	Pro	Glu	Lys	Leu	Phe	Gly	Lys	Thr	Leu	Asn	Lys	Val	Asp	Ile
		355					360					365			
Val	Glu	Leu	Arg	Asp	Ile	Ile	His	Glu	Phe	Ser	His	Thr	Lys	Gly	Tyr

370	375	380
Thr His Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu		
385	390	395
Asn Gly Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val		400
	405	410
Asn Gly Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp		415
	420	425
Gln Asp Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His		430
	435	440
Gln Val Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys		445
	450	455
Ala Gln Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln		460
465	470	475
Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn		480
	485	490
Ser Pro Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala		495
	500	505
Thr Ser Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr		510
	515	520
Thr Thr Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly		525
	530	535
Val Asn Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly		540
545	550	555
Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp		560
	565	570
Glu Lys Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe		575
	580	585
Asp Phe Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys		590
	595	600
Lys Val Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu		605
	610	615
Tyr Asn Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu		620
625	630	635
Asp Ile Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser		640
	645	650
Val Gly Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser		655
	660	665
Asn Asn Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser		670
	675	680
His Phe Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe		685
	690	700

<210> 181

<211> 397

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(344)

<400> 181

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Met Val

tat gaa gaa aat ttt gtg cat gcc ggg ttt gtg ctt att gcg tgc aat 104
 Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala Cys Asn
 5 10 15

 tat gcg gcc ttg tgc gcg ttg aat aaa aga cac agc gtg gtg gtt tct 152
 Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val Val Ser
 20 25 30

 aat aac atc aat ttt tat gcc ccc cta gaa ttg aat caa gaa gca ctc 200
 Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu Ala Leu
 35 40 45 50

 att aaa gcg caa gtg att caa gat ggc gtg aaa aaa gct gaa ata aaa 248
 Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu Ile Lys
 55 60 65

 ata gag gcg ttt gtg tta gac att cag gtt tta gag gga atg ata gaa 296
 Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu
 70 75 80

 att gtg gtg ttt gat aaa aag cct ttt aaa ttc aat ttt aaa gaa gag 344
 Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu
 85 90 95

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<211> 98

<212> PRT

<213> *Helicobacter pylori*

<400> 182

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 20 25 30
 Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu
 35 40 45
 Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu
 50 55 60
 Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met
 65 70 75 80
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 85 90 95
 Glu Glu

<210> 183

<211> 1261

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (51)...(1208)

<400> 183

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                                     Met Ala
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gaa aaa tta gag gaa act aat cct gaa tgg ttt gaa aaa tgg agg gaa      104
Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp Arg Glu
      5                      10                      15

aaa caa tac acc caa act ggc gaa tct aag cca tca aaa cga atc aaa      152
Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg Ile Lys
      20                      25                      30

gtt ttt aaa aac ttt acg gca ttt gat gac aga ttg tat aca att gaa      200
Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr Ile Glu
      35                      40                      45                      50

tgt aat tta aaa aat ctg gat acc cat caa aaa aag ttt gaa att tgt      248
Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu Ile Cys
      55                      60                      65

ggg gct ctg tat gac att tat gaa caa att ttt gat gaa aca cca agc      296
Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr Pro Ser
      70                      75                      80

ttg aaa ggg cgc gat tta gaa aca tac aaa gca caa gat ttg tca aag      344
Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu Ser Lys
      85                      90                      95

aaa ttc atg cat tta ggt ttt gaa cag atc tca aaa gat tta aac gac      392
Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu Asn Asp
      100                      105                      110

tct aga ttg aac gct tta ttg tgc tat gag gaa aaa gtc atg caa gct      440
Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met Gln Ala
      115                      120                      125                      130

ttg gct aaa aaa tac cct agt ttt tta caa gat ttg cat gat ata aaa      488
Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp Ile Lys
      135                      140                      145

aaa tac agg aat aaa gat aaa cac ggc gag aaa cca caa gat ggg tct      536
Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp Gly Ser
      150                      155                      160

tct tta acg aga gtg gaa tta gaa aga tac aga gat gga att tat ttt      584
Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile Tyr Phe
      165                      170                      175

cta gta gaa aat ctt tta aaa aac ccc ttg att aaa gag aga gaa aat      632
Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg Glu Asn
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180	185	190	
gct caa gaa gaa aaa cat tat aag aaa aat gca gag att gac gac cga			680
Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp Asp Arg			
195	200	205	210
tcc cag cta tca aac tta aac gca ccc aaa ccc tta ttt gaa tgt ttt			728
Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu Cys Phe			
	215	220	225
gta gga gtt aat ctg gcc aaa gcc aaa tat tat tct aaa aaa gaa gaa			776
Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys Glu Glu			
	230	235	240
aga gaa aaa gaa aag atg atc ttg aat ttt tgt aag ata ttt gaa att			824
Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe Glu Ile			
	245	250	255
att ctt ttt gaa gct atc caa aaa caa cca aag cct gat ttt aaa aat			872
Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe Lys Asn			
	260	265	270
aaa gac gag ctt tta ggg gat tat cct aat ctt aaa aat tta gat tct			920
Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu Asp Ser			
	275	280	285
tta aga gaa gtg agg gaa gac ttt ttg aaa aga gcg ttt aag aat gat			968
Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys Asn Asp			
	295	300	305
gaa gcg agt ttg gga gcg tat gtg tta gtg ttg ctt agc tgt aag tat			1016
Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys Lys Tyr			
	310	315	320
ttt gag agc gtg ttt gaa aaa gtt caa gaa tgg cta gat ttt atc gct			1064
Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe Ile Ala			
	325	330	335
agg ctt att gct ttg aga ggc cat gtg cac aag ata act aaa gaa ctt			1112
Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys Glu Leu			
	340	345	350
gaa aga tta gaa gaa gag gat tta gaa aaa ttg gaa aaa caa gca cta			1160
Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln Ala Leu			
	355	360	365
gaa tat ttt aat aaa ata gca aat aaa ata tat cta aag gag aaa cga			1208
Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu Lys Arg			
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tgagcgggaa tgaagaattg gagctaagag ccagagaaac tgagttggat aaa			1261
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<213> Helicobacter pylori

<400> 184

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Ile Lys Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr
 35          40          45
Ile Glu Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu
 50          55          60
Ile Cys Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr
 65          70          75          80
Pro Ser Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu
 85          90          95
Ser Lys Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu
100          105          110
Asn Asp Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met
115          120          125
Gln Ala Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp
130          135          140
Ile Lys Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp
145          150          155          160
Gly Ser Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile
165          170          175
Tyr Phe Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg
180          185          190
Glu Asn Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp
195          200          205
Asp Arg Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu
210          215          220
Cys Phe Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys
225          230          235          240
Glu Glu Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe
245          250          255
Glu Ile Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe
260          265          270
Lys Asn Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu
275          280          285
Asp Ser Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys
290          295          300
Asn Asp Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys
305          310          315          320
Lys Tyr Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe
325          330          335
Ile Ala Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys
340          345          350
Glu Leu Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln
355          360          365
Ala Leu Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu
370          375          380
Lys Arg
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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(359)

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 Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu
 5 10 15

gag caa ggt ttt att gaa gtc att aaa gga aaa caa aga tac ttg tat 152
 Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr
 20 25 30

gtg tat ctt aaa gat tac aga gaa tta gag ggc tat aac tcc gta gga 200
 Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly
 35 40 45 50

gct aat caa aag aac aat atc cca tcg cct ttt ttc tta cag att atg 248
 Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met
 55 60 65

cgt ttc tta gaa aag ttt gcc aaa gaa att gag aga gta aaa ata aca 296
 Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr
 70 75 80

aca aag aat gtg tta tgc ata ttc cta gcc aag agc tta tgc aaa gag 344
 Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu
 85 90 95

tta ata atg ttg ttt taaaattcac gcctatttct aatcctaata ccacttacac 399
 Leu Ile Met Leu Phe
 100

tttatcctac aag 412

<210> 186
 <211> 103
 <212> PRT
 <213> Helicobacter pylori

<400> 186
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 20 25 30
 Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser

Genomic coordinates																Position
Genomic coordinates																
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											Met	Gln				
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aaa	gcc	tta	tta	cat	tca	tca	ttc	ttt	tta	cct	tta	ttt	tta	tct	ttt	104
Lys	Ala	Leu	Leu	His	Ser	Ser	Phe	Phe	Leu	Pro	Leu	Phe	Leu	Ser	Phe	
		5				10				15						
tgt	atc	gct	gaa	gaa	aat	ggg	gcg	tat	gcg	agc	gtg	ggg	ttt	gaa	tat	152
Cys	Ile	Ala	Glu	Glu	Asn	Gly	Ala	Tyr	Ala	Ser	Val	Gly	Phe	Glu	Tyr	
		20				25				30						
tcc	att	agt	cat	gcc	gtt	gaa	cac	aat	aac	ccc	ttt	tta	aat	caa	gaa	200
Ser	Ile	Ser	His	Ala	Val	Glu	His	Asn	Asn	Pro	Phe	Leu	Asn	Gln	Glu	
35				40						45				50		
cgc	atc	caa	atc	att	tct	aac	gct	caa	aat	aaa	atc	tat	aaa	ctc	cat	248
Arg	Ile	Gln	Ile	Ile	Ser	Asn	Ala	Gln	Asn	Lys	Ile	Tyr	Lys	Leu	His	
				55				60						65		
caa	gtt	aaa	aat	gaa	atc	aca	agc	atg	cct	aaa	acc	ttt	gca	tat	atc	296
Gln	Val	Lys	Asn	Glu	Ile	Thr	Ser	Met	Pro	Lys	Thr	Phe	Ala	Tyr	Ile	
				70				75				80				
aac	aac	gct	tta	aaa	aac	aac	tcc	aaa	tta	acc	ccc	act	gaa	atg	caa	344
Asn	Asn	Ala	Leu	Lys	Asn	Asn	Ser	Lys	Leu	Thr	Pro	Thr	Glu	Met	Gln	
		85				90						95				
gcc	gaa	caa	tac	tac	ctc	caa	tcc	acc	ttt	caa	aac	att	gaa	aaa	ata	392
Ala	Glu	Gln	Tyr	Tyr	Leu	Gln	Ser	Thr	Phe	Gln	Asn	Ile	Glu	Lys	Ile	
100						105				110						
gta	atg	ctt	agc	ggg	ggc	gtt	tca	tct	aac	cca	caa	tta	gtc	caa	gcg	440
Val	Met	Leu	Ser	Gly	Gly	Val	Ser	Ser	Asn	Pro	Gln	Leu	Val	Gln	Ala	

115	120	125	130	
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135 140 145				
aac tta aga aat tta gaa gtg caa ttt gct caa tct caa aac cgc atg	536			
Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn Arg Met				
150 155 160				
ctt tct tct tta tct tct caa atc gct gcc att tca aat tcc tta aac	584			
Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser Leu Asn				
165 170 175				
gcg ctt gat cct aac tct tat tct aaa aac att tca agc atg tat ggg	632			
Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met Tyr Gly				
180 185 190				
gtg agt ttg agc gta ggt tat aag cat ttc ttt acc aag aaa aaa aat	680			
Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys Asn				
195 200 205 210				
caa ggg ttg cgc tat tac ttg ttt tat gac tat ggt tac act aat ttt	728			
Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe				
215 220 225				
ggg ttt gtg ggc aat ggc ttt gat ggt tta ggc aaa atg aat aac cat	776			
Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His				
230 235 240				
ctc tat ggg ctt ggg ata gac tat ctt tat aat ttc att gat aat gca	824			
Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala				
245 250 255				
aaa aaa cac tct agc gta ggt ttt tat ctg ggt ttt gct tta gcg ggg	872			
Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly				
260 265 270				
agt tcg tgg gta ggg agt ggt ttg agc atg tgg gtg agc caa acg gat	920			
Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp				
275 280 285 290				
ttt atc aac aat tac ttg acg ggc tat caa gct aaa atg cac acg agt	968			
Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser				
295 300 305				
ttt ttc cag atc cct ttg aat ttt ggg gtt cgt gtg aat gtc aat agg	1016			
Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg				
310 315 320				
cat aat ggc ttt gaa atg ggc ttg aaa atc cct tta gcg atg aat tcc	1064			
His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser				
325 330 335				
ttt tat gaa acg cat ggc aaa ggg cta aac act tcc ctc ttt ttc aaa	1112			

Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe Phe Lys
 340 345 350

cgc ctt gtc atg ttt aac gtg agt tac gtt tat agt ttt taggggggta 1161
 Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe
 355 360 365

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<211> 367

<212> PRT

<213> Helicobacter pylori

<400> 188

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 Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn
 35 40 45
 Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys
 50 55 60
 Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala
 65 70 75 80
 Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu
 85 90 95
 Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu
 100 105 110
 Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val
 115 120 125
 Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe
 130 135 140
 Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn
 145 150 155 160
 Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser
 165 170 175
 Leu Asn Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met
 180 185 190
 Tyr Gly Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys
 195 200 205
 Lys Asn Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr
 210 215 220
 Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn
 225 230 235 240
 Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp
 245 250 255
 Asn Ala Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu
 260 265 270
 Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln
 275 280 285
 Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His
 290 295 300
 Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val
 305 310 315 320

Asn	Arg	His	Asn	Gly	Phe	Glu	Met	Gly	Leu	Lys	Ile	Pro	Leu	Ala	Met
				325					330					335	
Asn	Ser	Phe	Tyr	Glu	Thr	His	Gly	Lys	Gly	Leu	Asn	Thr	Ser	Leu	Phe
			340					345					350		
Phe	Lys	Arg	Leu	Val	Met	Phe	Asn	Val	Ser	Tyr	Val	Tyr	Ser	Phe	
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 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
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cca cta ttg ttc act acg ggt tca tta ggg gcg gtt act tat gaa gtg	152
Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr Glu Val	
	20 25 30
cat gga gat ttt atc aat ttt gct aaa gtg ggt ttt aac cat tcg ccc	200
His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His Ser Pro	
	35 40 45 50
att aat cct gtt aaa ggt atc tat ccc aca gaa act ttt gtt aac ctt	248
Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val Asn Leu	
	55 60 65
acg ggt aag cta gag ggg tct gtg cat tta ggt agg gga tgg acc gtg	296
Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp Thr Val	
	70 75 80
aat tta ggc ggt gtt ttg ggc gga cag gct tat gat ggc act aag tat	344
Asn Leu Gly Gly Val Leu Gly Gly Gln Ala Tyr Asp Gly Thr Lys Tyr	
	85 90 95
gat agg tgg gcg aag gat ttt acc ccc cca agc tat tgg gat aaa act	392
Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp Lys Thr	
	100 105 110
tct tgc ggt act gat tct atg agt ctt tgt atg aat gcc act aaa atg	440
Ser Cys Gly Thr Asp Ser Met Ser Leu Cys Met Asn Ala Thr Lys Met	
	115 120 125 130
tgg cag caa tca ggg cca ggt ggc gtc att aac cct aga ggt att ggt	488

Trp	Gln	Gln	Ser	Gly	Pro	Gly	Gly	Val	Ile	Asn	Pro	Arg	Gly	Ile	Gly		
				135					140					145			
tgg	gaa	tac	atg	ggt	gag	tgg	aac	ggc	ttg	ttc	cct	aac	tac	tat	ccg	536	
Trp	Glu	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr	Tyr	Pro		
			150					155					160				
gct	aac	gcc	tac	ttg	cct	ggt	ggc	tca	agg	cgc	tat	caa	gtc	tat	aaa	584	
Ala	Asn	Ala	Tyr	Leu	Pro	Gly	Gly	Ser	Arg	Arg	Tyr	Gln	Val	Tyr	Lys		
		165						170				175					
gca	aat	ttg	acc	tat	gat	agc	gac	agg	gtc	cat	atg	gta	atg	ggg	cgt	632	
Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met	Gly	Arg		
	180						185				190						
ttt	gac	att	acc	gag	cag	gag	caa	atg	gat	tgg	att	tac	caa	ttg	ttc	680	
Phe	Asp	Ile	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln	Leu	Phe		
195					200					205					210		
caa	ggg	ttt	tat	ggg	act	ttc	aag	ctc	act	aag	aat	atg	aaa	ttc	ttg	728	
Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys	Phe	Leu		
				215					220					225			
ctc	ttt	agt	ggt	tgg	ggt	cgt	ggt	atc	gct	gat	ggt	cag	tgg	ttg	ttc	776	
Leu	Phe	Ser	Gly	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp	Leu	Phe		
			230					235					240				
cct	atc	tat	cgt	gaa	aag	cct	tgg	ggg	gtt	cat	aaa	gcg	ggt	att	att	824	
Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Val	His	Lys	Ala	Gly	Ile	Ile		
		245					250					255					
tat	cgc	cct	aca	aag	aat	ttg	atg	atc	cac	cct	tat	gtg	tat	ctt	atc	872	
Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr	Leu	Ile		
	260					265					270						
cca	atg	gta	ggc	aca	ttg	cct	ggt	gct	aaa	ata	gaa	tac	gat	acc	aat	920	
Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp	Thr	Asn		
275					280					285					290		
cct	gaa	ttt	agc	ggt	agg	ggc	att	agg	aac	aga	acg	act	ttc	tat	gcg	968	
Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Arg	Thr	Thr	Phe	Tyr	Ala		
			295						300					305			
ttg	tat	gac	tat	cgt	tgg	aat	aac	gct	gaa	tac	ggt	cgt	tac	gcg	ccc	1016	
Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr	Ala	Pro		
			310					315					320				
gct	cgt	tat	aac	act	tgg	gat	ccg	ttc	ttg	gat	aat	ggt	aag	tgg	cgt	1064	
Ala	Arg	Tyr	Asn	Thr	Trp	Asp	Pro	Phe	Leu	Asp	Asn	Gly	Lys	Trp	Arg		
		325					330					335					
ggc	ttg	caa	ggt	cct	ggt	ggt	gcg	acg	ctc	ctt	tta	cgc	cac	cat	ata	1112	
Gly	Leu	Gln	Gly	Pro	Gly	Gly	Ala	Thr	Leu	Leu	Leu	Arg	His	His	Ile		
	340					345					350						

gat att aac aac tac ttt gtg gtt ggt ggt gct tat ctc aac att ggt	1160
Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn Ile Gly	
355 360 365 370	
aac cct aac atg aac tta ggt act tgg ggt aac cct gtg gct gtt gat	1208
Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala Val Asp	
375 380 385	
ggg atc gaa caa tgg gtc ggt agt atc tat agc tta ggg ttt gcg ggg	1256
Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe Ala Gly	
390 395 400	
att gac aac att acc gat gct gac gcg ttc acc gag tat gtt aaa ggt	1304
Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val Lys Gly	
405 410 415	
gga ggc aag cat ggt aag ttt agt tgg agc gtt tat cag cgc ttc act	1352
Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg Phe Thr	
420 425 430	
acc gct cca agg gct ttg gaa tat ggt atc ggt atg tat cta gac tat	1400
Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu Asp Tyr	
435 440 445 450	
cag ttc agc aag cat gtt aaa gcg ggt ctc aaa ctc gta tgg tta gag	1448
Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp Leu Glu	
455 460 465	
ttc caa att cgt gcg ggt tac aac cct gga acc ggt ttc ctt ggg cca	1496
Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu Gly Pro	
470 475 480	
aac ggt cag ccg ctt aac ttg aat act ggt ttg ttt gag tct tca gcg	1544
Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser Ser Ala	
485 490 495	
ttc gct caa ggc cct caa aac atg ggc ggt atc gca aaa agc atc act	1592
Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser Ile Thr	
500 505 510	
caa gac aga agc cat ttg atg aca cac att agt tat agt ttc	1634
Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe	
515 520 525	
taagagagtt ctccccctat ctcttagata tgcctttttg tattttttatt tta	1687
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<211> 528	
<212> PRT	
<213> Helicobacter pylori	
<400> 190	
Met Lys Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe	
1 5 10 15	
Thr Leu Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr	

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Leu Glu Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu
 465 470 475 480
 Gly Pro Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser
 485 490 495
 Ser Ala Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser
 500 505 510
 Ile Thr Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe
 515 520 525

<210> 191
 <211> 412
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (51)...(359)

<400> 191
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 Met Phe
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 ttg ata cta tcg aat cca ttc ttc aac act tct gcc ata aaa ttc ttg 104
 Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu
 5 10 15

 ata ttg tcc ata ggc aag ttg aat ttt ttc cct aat att tca tta agt 152
 Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser
 20 25 30

 ccc atc att aac atc agg aag aac aaa aaa ttt aat atc ata gaa aac 200
 Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn
 35 40 45 50

 aaa tca ctg gat aaa cct gta aaa aga ttt gtt ccg cca ccc aac aaa 248
 Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys
 55 60 65

 gaa gct aaa att ttt ccc atg atc agt cct ttt att ttt ggt tgt gta 296
 Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val
 70 75 80

 agt tct tgc ttg ttc gga tct cta atg cgt gtt tta gta gga agc att 344
 Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile
 85 90 95

 tca caa tgg cat acc taaagctact aagaaaattc ttgaatctat tggttaagatt 399
 Ser Gln Trp His Thr
 100

 actcatgaaa tca 412

<210> 192

<211> 103
 <212> PRT
 <213> Helicobacter pylori

<400> 192
 Met Phe Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys
 1 5 10 15
 Phe Leu Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser
 20 25 30
 Leu Ser Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile
 35 40 45
 Glu Asn Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro
 50 55 60
 Asn Lys Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly
 65 70 75 80
 Cys Val Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly
 85 90 95
 Ser Ile Ser Gln Trp His Thr
 100

<210> 193
 <211> 447
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (67)...(405)

<400> 193
 tccaatccgt ctaatatctc tttattttcg ctcaattctt taaccataac gggtttttta 60
 ggcgctt gtg ggg gtt act ggg cta aag ttt gga gcg ttt tgc act tct 108
 Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser
 1 5 10
 ttt tct tct ttt ttt aga ttt tcc ttt atc att tct tct atc ctt cct 156
 Phe Ser Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro
 15 20 25 30
 tct atc att tct tct tgc gtg ttt tct tgt ggg ttt tct tct ttt tta 204
 Ser Ile Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu
 35 40 45
 ggg tgg ttg ggg gtt ttt tgg ttt tct gtt ttg ttg tca ttt tct att 252
 Gly Trp Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile
 50 55 60
 atg ggt gca agt gtg ggc atg ata ggt ttg ggc gtg gtg ggc gta aga 300
 Met Gly Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg
 65 70 75
 gtt tct ttt gta ggc gtg ggt tct ctt tct tta gtt tct tgt tta att 348
 Val Ser Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile
 80 85 90

tct ttt aaa ggg ggg tta gtg ggg tta gtc aaa tca tca aat cgg ttt	396
Ser Phe Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe	
95 100 105 110	

ctt tta ggg taaatgggtgt aatgggtagg ggggtgggag gaaatttgga	445
Leu Leu Gly	

ct	447
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<210> 194
 <211> 113
 <212> PRT
 <213> Helicobacter pylori

<400> 194

Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser Phe Ser	
1 5 10 15	
Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro Ser Ile	
20 25 30	
Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu Gly Trp	
35 40 45	
Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile Met Gly	
50 55 60	
Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg Val Ser	
65 70 75 80	
Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile Ser Phe	
85 90 95	
Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe Leu Leu	
100 105 110	
Gly	

<210> 195
 <211> 1180
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1127)

<400> 195

ccaagaaaga gtataatagc gcataagaat ttaactgatg aagagggttta atg cta	56
Met Leu	
1	
gaa aat aga gtt aag acc aag caa att ttt atc ggt ggc gtg gcc ata	104
Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile	
5 10 15	
ggg ggt gat gct ccc ata agc acg caa agc atg acc ttt agc aaa acc	152
Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr	

20	25	30	
gct gat att gaa agc act aaa aat caa att gac aga ctc aaa ctc gcc			200
Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala			
35	40	45	50
ggg gcc gat tta gtg agg gtg gcg gtg agt aat gaa aag gac gct cta			248
Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu			
	55	60	65
gcc tta aaa gaa ttg aaa aaa gtg tcc cct ttg cct tta atc gct gat			296
Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp			
	70	75	80
att cat ttc cat tat aaa ttc gct ctc att gcc gct caa agc gtg gat			344
Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp			
	85	90	95
gcg atc agg att aac ccc gga aac atc ggc tct aaa gag aag atc aaa			392
Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys			
	100	105	110
gcg gtg gtt gat gct tgt aaa gaa aaa aac att cct ata aga att ggc			440
Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly			
115	120	125	130
gtg aat gct ggg agt tta gaa aag cag ttt gat caa aaa tac gga ccc			488
Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro			
	135	140	145
acc cca aaa ggc atg gta gaa agc gct ttg tat aac gcc aaa ctt tta			536
Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys Leu Leu			
	150	155	160
gaa gat ttg gat ttt acc aat ttt aag att tct tta aaa gcg agc gat			584
Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala Ser Asp			
	165	170	175
gtg att cgc acc ata gaa gct tac agg atg ctt cgc cct ctt gtg atc			632
Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu Val Ile			
	180	185	190
tat cct ttc cat ttg ggg gtt acg gag gcg ggg aat ctt ttt agc tcc			680
Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe Ser Ser			
195	200	205	210
agt atc aaa tcc gct atg gct tta ggg ggg ctt tta atg gag ggc att			728
Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu Gly Ile			
	215	220	225
ggg gat acg atg cgc gta tcc atc aca ggg gaa tta gaa aat gaa atc			776
Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn Glu Ile			
	230	235	240
aaa gtg gcc aga gca att tta cgc cat agc ggg cgg ttg aaa gaa ggg			824

Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys Glu Gly
 245 250 255

att aat tgg att tct tgc ccc act tgc ggg cgc att gaa gcc aat tta 872
 Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala Asn Leu
 260 265 270

gtg gat atg gcg atc aag gta gaa aaa cgc tta agc cac atc aaa acc 920
 Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile Lys Thr
 275 280 285 290

cct tta gac att agc gtg atg ggt tgc gtg gtg aat gct ttg ggt gaa 968
 Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu Gly Glu
 295 300 305

gcc aag cat gca gac atg gcg atc gct ttt ggg aat cgc agc ggt ttg 1016
 Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser Gly Leu
 310 315 320

atc att aaa gag ggt aaa gtc att cac aaa ctg gct gaa aag gat tta 1064
 Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys Asp Leu
 325 330 335

ttt gaa act ttt gtg ata gaa gtg gaa aat tta gct aaa gaa aga gaa 1112
 Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu Arg Glu
 340 345 350

aaa agt tta aag gat taggcatgat caataagttt aaaaattttg tgagcaacta 1167
 Lys Ser Leu Lys Asp
 355

ccagcaatct aac 1180

<210> 196
 <211> 359
 <212> PRT
 <213> *Helicobacter pylori*

<400> 196
 Met Leu Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val
 1 5 10 15
 Ala Ile Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser
 20 25 30
 Lys Thr Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys
 35 40 45
 Leu Ala Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp
 50 55 60
 Ala Leu Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile
 65 70 75 80
 Ala Asp Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser
 85 90 95
 Val Asp Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys
 100 105 110
 Ile Lys Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg
 115 120 125

Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr
 130 135 140
 Gly Pro Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys
 145 150 155 160
 Leu Leu Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala
 165 170 175
 Ser Asp Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu
 180 185 190
 Val Ile Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe
 195 200 205
 Ser Ser Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu
 210 215 220
 Gly Ile Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn
 225 230 235 240
 Glu Ile Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys
 245 250 255
 Glu Gly Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala
 260 265 270
 Asn Leu Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile
 275 280 285
 Lys Thr Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu
 290 295 300
 Gly Glu Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser
 305 310 315 320
 Gly Leu Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys
 325 330 335
 Asp Leu Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu
 340 345 350
 Arg Glu Lys Ser Leu Lys Asp
 355

<210> 197
 <211> 1399
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (51)...(1346)

<400> 197
 gcctatgaaa tcttaaagcg ttatccggct aaagcaaagg tataaataac atg aaa 56
 Met Lys
 1

 aaa ttt tta atc act tta tta tta gga gtt ttt atg ggg tta caa gcg 104
 Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala
 5 10 15

 agc gct ttg aca cac caa gaa atc aat caa gct aaa gtc cct gtg att 152
 Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile
 20 25 30

 tat gaa gaa aac cat ttg ttg cct atg ggg ttt atc cat tta gcc ttt 200

Tyr	Glu	Glu	Asn	His	Leu	Leu	Pro	Met	Gly	Phe	Ile	His	Leu	Ala	Phe		
35					40					45					50		
agg	ggg	ggt	ggg	agc	tta	agc	gat	aaa	aac	cag	ttg	ggt	ttg	gcg	aaa	248	
Arg	Gly	Gly	Gly	Ser	Leu	Ser	Asp	Lys	Asn	Gln	Leu	Gly	Leu	Ala	Lys		
				55				60						65			
tta	ttc	gcg	caa	ggt	tta	aac	gaa	ggc	act	aaa	gag	ctt	ggt	gcg	gtg	296	
Leu	Phe	Ala	Gln	Val	Leu	Asn	Glu	Gly	Thr	Lys	Glu	Leu	Gly	Ala	Val		
			70					75					80				
ggg	ttt	gcg	caa	ctt	tta	gag	caa	aaa	gcg	atc	agt	ttg	aat	gtg	gat	344	
Gly	Phe	Ala	Gln	Leu	Leu	Glu	Gln	Lys	Ala	Ile	Ser	Leu	Asn	Val	Asp		
		85					90					95					
acc	agc	aca	gaa	gat	ttg	caa	atc	act	tta	gaa	ttt	tta	aaa	gaa	tac	392	
Thr	Ser	Thr	Glu	Asp	Leu	Gln	Ile	Thr	Leu	Glu	Phe	Leu	Lys	Glu	Tyr		
	100					105					110						
gaa	gat	gaa	gcc	att	acg	cgc	tta	aaa	gag	ctt	tta	aaa	tcc	cct	aat	440	
Glu	Asp	Glu	Ala	Ile	Thr	Arg	Leu	Lys	Glu	Leu	Leu	Lys	Ser	Pro	Asn		
115					120				125						130		
ttc	acg	caa	aac	gct	tta	gaa	aaa	gtc	aaa	acc	caa	atg	tta	gcc	gca	488	
Phe	Thr	Gln	Asn	Ala	Leu	Glu	Lys	Val	Lys	Thr	Gln	Met	Leu	Ala	Ala		
			135					140						145			
ctt	tta	caa	aaa	gaa	agc	gat	ttt	gac	tat	ttg	gct	aaa	ttg	act	tta	536	
Leu	Leu	Gln	Lys	Glu	Ser	Asp	Phe	Asp	Tyr	Leu	Ala	Lys	Leu	Thr	Leu		
		150						155					160				
aag	caa	gag	ctt	ttt	gct	aac	acc	cct	tta	gct	aac	gca	gcc	tta	ggc	584	
Lys	Gln	Glu	Leu	Phe	Ala	Asn	Thr	Pro	Leu	Ala	Asn	Ala	Ala	Leu	Gly		
	165					170					175						
act	aaa	gag	agc	att	caa	aaa	atc	aag	cta	gac	gat	ttg	aaa	cag	caa	632	
Thr	Lys	Glu	Ser	Ile	Gln	Lys	Ile	Lys	Leu	Asp	Asp	Leu	Lys	Gln	Gln		
	180					185				190							
ttt	gct	aag	gtc	ttt	gaa	ctc	aat	aag	ctc	gtg	gtg	gtg	ctt	ggg	ggc	680	
Phe	Ala	Lys	Val	Phe	Glu	Leu	Asn	Lys	Leu	Val	Val	Val	Leu	Gly	Gly		
195					200				205					210			
gat	ttg	aaa	atc	gat	caa	acc	ctt	aag	cgt	ttg	aat	aac	gcc	ctt	aat	728	
Asp	Leu	Lys	Ile	Asp	Gln	Thr	Leu	Lys	Arg	Leu	Asn	Asn	Ala	Leu	Asn		
				215				220					225				
ttc	ttg	cca	caa	ggt	aaa	gcg	tat	gaa	gag	cct	tat	ttt	gaa	acg	agc	776	
Phe	Leu	Pro	Gln	Gly	Lys	Ala	Tyr	Glu	Glu	Pro	Tyr	Phe	Glu	Thr	Ser		
		230					235					240					
gat	aaa	aaa	agc	gaa	aaa	gtc	ctc	tat	aaa	gac	act	gag	cag	gct	ttc	824	
Asp	Lys	Lys	Ser	Glu	Lys	Val	Leu	Tyr	Lys	Asp	Thr	Glu	Gln	Ala	Phe		
	245					250						255					

gtg tat ttt ggt gcg ccc ttt aaa atc aag gat tta aaa cag gat tta	872
Val Tyr Phe Gly Ala Pro Phe Lys Ile Lys Asp Leu Lys Gln Asp Leu	
260 265 270	
gcg aaa tct aaa gtc atg atg ttt gtg ctt ggt ggg ggg ttt ggc tct	920
Ala Lys Ser Lys Val Met Met Phe Val Leu Gly Gly Gly Phe Gly Ser	
275 280 285 290	
cgt tta atg gaa aaa atc agg gtt caa gag gga tta gct tat agc gtg	968
Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly Leu Ala Tyr Ser Val	
295 300 305	
tat atc cgc tcc aat ttt tct aaa gtg gcg cat ttt gcg agc ggg tat	1016
Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala Ser Gly Tyr	
310 315 320	
ttg caa acc aag ctc agc act caa act aaa agc gtt gcc tta gtt aaa	1064
Leu Gln Thr Lys Leu Ser Thr Gln Thr Lys Ser Val Ala Leu Val Lys	
325 330 335	
aaa atc gtt aag gaa ttt ata gaa aaa ggc atg acg caa caa gaa tta	1112
Lys Ile Val Lys Glu Phe Ile Glu Lys Gly Met Thr Gln Gln Glu Leu	
340 345 350	
gac gac gct aaa aag ttt tta cta ggc tct gag cct tta agg aat gaa	1160
Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg Asn Glu	
355 360 365 370	
acg atc tct agc cgc ttg aac acc act tac aat tat ttt tat tta ggt	1208
Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly	
375 380 385	
ttg cct tta aat ttt aac caa acg ctg ctc aat caa atc caa aaa atg	1256
Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln Lys Met	
390 395 400	
agt ttg aaa gaa atc aat gat ttc att aaa gcc cac acc gaa atc aac	1304
Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu Ile Asn	
405 410 415	
gac ttg act ttt gct att gtg agc aat aaa aag aag gac aaa	1346
Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Lys Asp Lys	
420 425 430	
tgatgccatt tgaagctgta atcgggctag aagtcctatgt ccaactcaac acc	1399
<210> 198	
<211> 432	
<212> PRT	
<213> Helicobacter pylori	
<400> 198	
Met Lys Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu	
1 5 10 15	
Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro	

$\langle 210 \rangle$	199
$\langle 211 \rangle$	574

<212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(521)

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<400> 199
gaagagccag aaaatttaga aacctcttcg gcacaaaatt tgtttgagtg atg cgt      56
                                         Met Arg
                                         1

ttc ttt tca ttc ttt tat ttt tta ttt tat ttt tta ggg gtt tct ttg      104
Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val Ser Leu
      5              10              15

caa gct ctc agc ccc cta gaa gat caa gaa ttt tta att tcg tac cgc      152
Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser Tyr Arg
      20              25              30

ttg aaa atc gtt gat tct aga gtg atg ggc gaa gag tat tct gtc tct      200
Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser Val Ser
      35              40              45              50

aaa cct atc gtt agc cgc att aaa aca gcc ccc tat gtt tta gac tat      248
Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu Asp Tyr
              55              60              65

cat tgc tcc atc atc act cgt aac tta ccc aat ttg aaa aac ccc ttg      296
His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn Pro Leu
              70              75              80

ctc cca ata aag tta gaa cgc ttc ctt tta gaa atc gcg tta aaa aaa      344
Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu Lys Lys
      85              90              95

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Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val Ala Ile
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acg cat tat gat cat agc tat aaa aac ggc acc act acc aca agc att      440
Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr Ser Ile
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ctt gcc ctc aaa gcc tta agc gtt aga gcg agt tta gtg gga gat gcg      488
Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly Asp Ala
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 Tyr Arg Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser
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 Val Ser Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu
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 Asp Tyr His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn
 65 70 75 80
 Pro Leu Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu
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 Lys Lys Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val
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 Ala Ile Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr
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 5 10 15
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 Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser Leu Lys
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 Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val Asp Ser
 35 40 45 50
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 His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr Asn Ile

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Lys	Ser	Val	Val	Leu	Lys	Thr	Lys	Asn	Gly	Gln	Tyr	Phe	Val	Ser	Pro															
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Asn Arg Asp Asn Phe Ala Gln Lys Tyr Gln Ile Lys Ser Gly Ala Asp
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 Asp Ser His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
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 Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp
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 Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
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 Lys Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
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 Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
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 Asp Ser Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser
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 Glu Lys Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly
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 Ala Arg Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu
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 Leu Pro Pro Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr
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 Lys Gly Glu Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly
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Val	Ile	Ile	Glu	His	Lys	Asn	Gly	Ile	Arg	Thr	Ile	Tyr	Ser	Gln	Leu	
	340					345				350						

gat aaa atc gct ccc acc att aaa agc ggc atg cgg atc caa aaa ggc 1160
 Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly
 355 360 365 370

tat gtt tta ggg cgc att gat caa cgc ttg ggc ttt gaa gtt acc atg 1208
 Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met
 375 380 385

aga gaa aaa cac atc aac ccc tta gaa ctc atc gca cgc aat 1250
 Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn
 390 395 400

taaacaaatc gtttttattg ccgatattgg ctaaagaatt tatgcaaaca aat 1303

<210> 206

<211> 400

<212> PRT

<213> Helicobacter pylori

<400> 206

Met Tyr Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn
 1 5 10 15
 Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr
 20 25 30
 Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu
 35 40 45
 Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu
 50 55 60
 Met Glu Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg
 65 70 75 80
 Asn Glu Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser
 85 90 95
 Leu Asp His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe
 100 105 110
 Asp Thr Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln
 115 120 125
 Asn Leu Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn
 130 135 140
 Leu His Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu
 145 150 155 160
 Lys Glu Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys
 165 170 175
 Ile Ser Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys
 180 185 190
 Ser Leu Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp
 195 200 205
 Tyr Ala Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln
 210 215 220
 Asn Leu Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg
 225 230 235 240
 Glu Asn Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu
 245 250 255
 Val Lys Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr
 260 265 270
 Asn Gly Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln

ttccactcta ggc

361

<210> 208

<211> 86

<212> PRT

<213> Helicobacter pylori

<400> 208

Met	Ser	Gly	Cys	Ala	Ser	Ser	Ser	Pro	Thr	Gly	Thr	Leu	Ile	Thr	Met
1				5					10					15	
Val	Thr	Met	Pro	Val	Ser	Gly	Asn	Asp	Ala	Gln	Tyr	Ser	Lys	Glu	Gly
			20					25					30		
Arg	Ala	Ser	Cys	Trp	Ser	Val	Phe	Ser	Leu	Val	Ala	Ala	Gly	Asn	Cys
		35					40					45			
Ser	Val	Glu	Lys	Ala	Ala	Lys	Ser	Gly	Gly	Val	Thr	Lys	Ile	Lys	Met
	50					55					60				
Val	Ser	Arg	Glu	Thr	Asn	Asn	Phe	Leu	Gly	Ile	Val	Gly	Lys	Tyr	Thr
65					70					75					80
Thr	Ile	Val	Gln	Gly	Asp										
				85											

<210> 209

<211> 1564

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1511)

<400> 209

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	Met Ile
	1
gaa tgg atg caa aat cat aga aaa tat tta gtg gtt aca ata tgg ata	104
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile	
	5 10 15
agc acg atc gct ttt att gcc gct ggg atg ata ggc tgg ggg caa tac	152
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr	
	20 25 30
agc ttt tct tta gat agc gat agc gct gcc aaa gtg gga cag att aag	200
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys	
	35 40 45 50
att tct caa gaa gaa tta gcc caa gaa tac cgc cgc ctt aaa gac gca	248
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala	
	55 60 65
tat gct gag tct atc cct gat ttt aaa gaa ctc acc aaa gat caa atc	296
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Lys Asp Gln Ile	
	70 75 80

aaa gcc atg cat tta gaa aaa agc gct tta gat tcg ctc atc aat caa	344
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln	
85 90 95	
gcc tta ttg aga aat ctc gct tta gat tta ggg ctt ggc gct aca aag	392
Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys	
100 105 110	
caa gaa gtg gcg aaa gag atc aga aaa acg agc gtt ttc caa aaa gat	440
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln Lys Asp	
115 120 125 130	
ggc gtt ttt gat gaa gaa ttg tat aaa aat atc tta aag caa agc cat	488
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His	
135 140 145	
tac cgc ccc aaa cat ttt gaa gaa agc gtt gaa agg ctt tta atc ctt	536
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu	
150 155 160	
caa aaa atc agc act cta ttc ccc aaa acc act acc cct ttg gag caa	584
Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln	
165 170 175	
tcc agc cta tcg ctt tgg gca aaa ttg caa gac aaa tta gac att ctt	632
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu	
180 185 190	
atc cta aac cct agt gat gtt aaa atc tct ctt aat gaa gaa gag atg	680
Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met	
195 200 205 210	
aaa aaa tat tac gag tcc cat aaa aag gat ttt aaa aag ccc acg agc	728
Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro Thr Ser	
215 220 225	
ttt aaa aca cgc tct tta tat ttt gac gct agt ttg gaa aaa cct gat	776
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Pro Asp	
230 235 240	
ttg aag gag ttg gag gaa tac tac cat aaa aac aag gtg tct tat ttg	824
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu	
245 250 255	
gac aaa gag ggg aaa ttg cag gat ttt aaa agc gtt caa gag caa gtc	872
Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln Val	
260 265 270	
aag cat gat tta agc atg caa aaa gcg aat gaa aaa gcc tta agg agc	920
Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser	
275 280 285 290	
tat atc gct cta aaa aaa gcg aac gcg caa aac tac acc aca caa gat	968
Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp	

295	300	305	
ttt gaa gag aac aac tcc ccc tat act gct gaa atc acg caa aaa ctc			1016
Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu			
310	315	320	
acc gct ctc aaa ccc ctt gaa atc cta aag cca gag cct ttt aaa gat			1064
Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp			
325	330	335	
ggg ttt att gtg gtg caa ctc atc tct caa att aaa gac gaa ttg caa			1112
Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln			
340	345	350	
aat ttt aat gaa gct aaa agc gct ctt aaa acc cgc cta act caa gaa			1160
Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu			
355	360	365	370
aaa acc ctt atg gcg ttg caa act tta gcc aaa gaa aag ctt aag gat			1208
Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp			
375	380	385	
ttt aag ggc aaa agc gtg ggc tat gta agc cct aat ttt gga ggc act			1256
Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr			
390	395	400	
att agt gag ctt aac caa gaa gaa agt gct aag ttt atc aac gct ctt			1304
Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu			
405	410	415	
ttt aac cgc cag gaa aaa aag ggg ttt atc gct att aat aat aaa gtg			1352
Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val			
420	425	430	
gtg ctc tat caa atc aca gaa caa aat ttc aac cac tca ttt agt gca			1400
Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala			
435	440	445	450
gaa gaa agc cag tat atg cag cgt tta gtc aat aac act aaa acg gat			1448
Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp			
455	460	465	
ttt ttt gat aaa gcg ttg ata gaa gaa ttg aaa aaa cgc tat aag ata			1496
Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile			
470	475	480	
gtc aaa tac att caa taaatgcaag gggaaatcat ggaacataaaa gaaatcgтта			1551
Val Lys Tyr Ile Gln			
485			
taggggttga tct			1564
<210> 210			
<211> 487			
<212> PRT			

<400> 210

-273-

Ala Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn
420 425 430
Lys Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe
435 440 445
Ser Ala Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys
450 455 460
Thr Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr
465 470 475 480
Lys Ile Val Lys Tyr Ile Gln
485

<210> 211
<211> 1435
<212> DNA
<213> Helicobacter pylori

<220>
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<222> (51)...(1382)

<400> 211
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Met Lys
1
cat ttt tct gtt aaa aga ctt tta ggg ctt agt tct gtc ttg tta gtc 104
His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu Leu Val
5 10 15
act tta gga gcg agc atg cac gca caa tct tac tta ccc aaa cat gag 152
Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys His Glu
20 25 30
agc gtt acc tta aaa aac ggg ttg caa gtc gtg agc gtc ccc cta gaa 200
Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro Leu Glu
35 40 45 50
aat aaa acc ggg gtt ata gaa gtg gat gtg ctt tat aaa gtc ggc tct 248
Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val Gly Ser
55 60 65
aga aac gaa acc atg gga aag agc ggg atc gct cac atg tta gag cat 296
Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu Glu His
70 75 80
ttg aat ttt aaa agc acc aaa aac ctt aaa gcc ggc gaa ttt gat aaa 344
Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe Asp Lys
85 90 95
atc gtt aag cgt ttt ggg ggc gtg agt aac gct tct acg agt ttt gat 392
Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser Phe Asp
100 105 110
att acg cgc tac ttc att aaa acc agt cag gct aac ttg gat aag tct 440

Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp Lys Ser	
115 120 125 130	
tta gaa ttg ttc gct gaa acc atg ggt tca ttg aat tta aaa gaa gat	488
Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys Glu Asp	
135 140 145	
gag ttt ttg cct gag cgt caa gtg gtc gct gaa gaa agg cga tgg cgc	536
Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg Trp Arg	
150 155 160	
act gat aat tcc cct atc ggc atg ctt tat ttc cgc ttt ttt aac acc	584
Thr Asp Asn Ser Pro Ile Gly Met Leu Tyr Phe Arg Phe Phe Asn Thr	
165 170 175	
gct tat gtc tat cac ccc tac cat tgg acg ccc att ggt ttt atg gat	632
Ala Tyr Val Tyr His Pro Tyr His Trp Thr Pro Ile Gly Phe Met Asp	
180 185 190	
gat att caa aat tgg act tta aaa gac att aaa aaa ttc cat tcg ctc	680
Asp Ile Gln Asn Trp Thr Leu Lys Asp Ile Lys Lys Phe His Ser Leu	
195 200 205 210	
tat tat cag cct aaa aac gct atc gtt ttg gtg gta ggc gat gtc aat	728
Tyr Tyr Gln Pro Lys Asn Ala Ile Val Leu Val Val Gly Asp Val Asn	
215 220 225	
tcc caa aag gtt ttt gaa ttg agt aaa aag cat ttt gaa tcc tta aaa	776
Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser Leu Lys	
230 235 240	
aac ctt gat gaa aaa gct atc ccc acc cct tac atg aaa gag cct aag	824
Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu Pro Lys	
245 250 255	
caa gat gga gcc aga acg gca gtc gtg cat aaa gat ggg gtc cat tta	872
Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val His Leu	
260 265 270	
gaa tgg gtg gcc ctt ggg tat aaa gtg cct gct ttc aag cat aaa gat	920
Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His Lys Asp	
275 280 285 290	
caa gtc gcc tta gac gca cta agt agg ctt tta ggc gaa ggc aaa agc	968
Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly Lys Ser	
295 300 305	
tcg tgg ttg caa agc gaa tta gtg gat aaa aaa cgc ttg gct tct caa	1016
Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala Ser Gln	
310 315 320	
gct ttc tcg cac aac atg caa tta caa gat gaa agc gtg ttt tta ttc	1064
Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe Leu Phe	
325 330 335	

att gcg ggg ggt aat cct aat gtc aaa gcc gaa gcc tta caa aaa gaa 1112
 Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln Lys Glu
 340 345 350

atc gta gcg ctt tta gaa aag ctg aaa aaa ggc gaa atc act caa gcg 1160
 Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr Gln Ala
 355 360 365 370

gaa tta gac aag ctc aaa atc aat caa aaa gct gac ttt att tct aat 1208
 Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile Ser Asn
 375 380 385

tta gaa agt tct agc gat gtt gcg ggg ctt ttt gcg gac tat tta gtg 1256
 Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr Leu Val
 390 395 400

caa aac gat att caa ggc ttg acg gat tac cag cga caa ttt ttg gat 1304
 Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe Leu Asp
 405 410 415

tta aaa gtg agc gat ttg gtg cgt gtg gcc aat gaa tat ttt aaa gac 1352
 Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe Lys Asp
 420 425 430

acc caa tca acc acc gtg ttt ttg aaa cct taaaagagcc ttataacatg 1402
 Thr Gln Ser Thr Thr Val Phe Leu Lys Pro
 435 440

caatttcatt catctagcgc gttgattacg cct 1435

<210> 212
 <211> 444
 <212> PRT
 <213> *Helicobacter pylori*

<400> 212
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 Leu Val Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys
 20 25 30
 His Glu Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro
 35 40 45
 Leu Glu Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val
 50 55 60
 Gly Ser Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu
 65 70 75 80
 Glu His Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe
 85 90 95
 Asp Lys Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser
 100 105 110
 Phe Asp Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp
 115 120 125
 Lys Ser Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys
 130 135 140
 Glu Asp Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg

5	10	15	
ggc aat atc caa atc cag agc atg ccc aaa gtt aaa gag cga gtg agt			152
Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser			
20	25	30	
gtc ccc tct aaa gac gat acg gat cta ttc tta cca cga ttc tat			197
Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr			
35	40	45	
taaggactct attaaggcgg tggatgaatat ctccactgaa aagaagatta aaa			250
<210> 214			
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<212> PRT			
<213> Helicobacter pylori			
<400> 214			
Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu			
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Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg			
20	25	30	
Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe			
35	40	45	
Tyr			
<210> 215			
<211> 328			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (51)...(275)			
<400> 215			
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		Met Gln	
		1	
cag cgt cat tta ggc cct tta aaa gtg ggt gca tta gct cta ggg tgc			104
Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu Gly Cys			
5	10	15	
atg ggc atg act tat ggg tat ggg gaa gtc cat gat aaa aag cag atg			152
Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys Gln Met			
20	25	30	
gtt aaa ctt atc cat aag gct ttg gaa ttg ggt att aac ttt ttt gac			200
Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe Phe Asp			
35	40	45	50
act gca gag gct tat ggg gaa gat aat gaa aag ctt tta ggc gaa cga			248

55										60										65										
aat	att	gat	gtg	aaa	agc	gtc	aat	act	agg	gat	aga	aaa	aga	gat	aac	296														
Asn	Ile	Asp	Val	Lys	Ser	Val	Asn	Thr	Arg	Asp	Arg	Lys	Arg	Asp	Asn															
				70					75					80																
cac	ttg	aaa	aca	gcg	gac	ttt	ttt	gat	gtg	gta	aaa	tac	ccc	aaa	ggg	344														
His	Leu	Lys	Thr	Ala	Asp	Phe	Phe	Asp	Val	Val	Lys	Tyr	Pro	Lys	Gly															
				85					90					95																
agc	ttt	aaa	atg	acc	aaa	tac	gaa	gat	ggg	aaa	atc	tat	ggg	gat	ttg	392														
Ser	Phe	Lys	Met	Thr	Lys	Tyr	Glu	Asp	Gly	Lys	Ile	Tyr	Gly	Asp	Leu															
				100					105					110																
act	ctt	cgt	ggc	gta	acc	aag	cct	gtc	gta	ttg	gaa	gcc	aaa	atc	caa	440														
Thr	Leu	Arg	Gly	Val	Thr	Lys	Pro	Val	Val	Leu	Glu	Ala	Lys	Ile	Gln															
				115					120					125																
gcc	ccc	tta	caa	aac	ccc	atg	aat	aaa	aaa	gaa	ttc	atg	gtg	tta	caa	488														
Ala	Pro	Leu	Gln	Asn	Pro	Met	Asn	Lys	Lys	Glu	Phe	Met	Val	Leu	Gln															
				135					140					145																
gct	gaa	ggc	aaa	atc	aac	cgc	aag	gat	ttt	ggg	atc	ggg	aaa	acc	ttt	536														
Ala	Glu	Gly	Lys	Ile	Asn	Arg	Lys	Asp	Phe	Gly	Ile	Gly	Lys	Thr	Phe															
				150					155					160																
agc	gat	gct	gtc	gtt	gga	gat	gag	gta	aag	att	gag	ctc	aaa	cta	gaa	584														
Ser	Asp	Ala	Val	Val	Gly	Asp	Glu	Val	Lys	Ile	Glu	Leu	Lys	Leu	Glu															
				165					170					175																
gct tac gcc caa taatcgtttt gcaagagata gatattcttct tctcttgcgt																636														
Ala Tyr Ala Gln																														
180																														
ttttctaaca gca																649														
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1					5					10					15															
Ala	Lys	Pro	Tyr	Thr	Ile	Asp	Lys	Ala	Asn	Ser	Ser	Val	Trp	Phe	Glu															
				20					25					30																
Val	Lys	His	Phe	Thr	Phe	Asn	Glu	Thr	Arg	Gly	Ala	Phe	Asp	Asn	Phe															
				35					40					45																
Asp	Gly	Lys	Ile	Asp	Leu	Glu	Pro	Asn	Thr	Lys	Met	Leu	Ser	Val	Phe															
				50					55					60																
Glu	Gly	Asn	Ile	Asp	Val	Lys	Ser	Val	Asn	Thr	Arg	Asp	Arg	Lys	Arg															
				65					70					75																
Asp	Asn	His	Leu	Lys	Thr	Ala	Asp	Phe	Phe	Asp	Val	Val	Lys	Tyr	Pro															
				85					90					95																
Lys	Gly	Ser	Phe	Lys	Met	Thr	Lys	Tyr	Glu	Asp	Gly	Lys	Ile	Tyr	Gly															

	100		105		110										
Asp	Leu	Thr	Leu	Arg	Gly	Val	Thr	Lys	Pro	Val	Val	Leu	Glu	Ala	Lys
	115		120		125										
Ile	Gln	Ala	Pro	Leu	Gln	Asn	Pro	Met	Asn	Lys	Lys	Glu	Phe	Met	Val
	130		135		140										
Leu	Gln	Ala	Glu	Gly	Lys	Ile	Asn	Arg	Lys	Asp	Phe	Gly	Ile	Gly	Lys
145			150		155				160						
Thr	Phe	Ser	Asp	Ala	Val	Val	Gly	Asp	Glu	Val	Lys	Ile	Glu	Leu	Lys
			165		170				175						
Leu	Glu	Ala	Tyr	Ala	Gln										
	180														

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 <211> 478
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(425)

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aag tta gcc gct tta ttt tta gta agc gtg ttg ggg gtt atg ggt tta	104
Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu	
	5 10 15
aac gca tgg gag caa acc cta aaa gct aat gac ttg gaa gtg aaa atc	152
Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile	
	20 25 30
aaa tcc gtg ggt aac ccc att aaa ggc gat aac act ttc att ctc agc	200
Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser	
	35 40 45 50
ccc act tta aaa ggt aag gct tta gaa aaa gct atc gtt agg gtg cag	248
Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln	
	55 60 65
ttt atg atg cct gaa atg ccc ggc atg cca gcg atg aaa gaa atg gcg	296
Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala	
	70 75 80
caa gtg agt gaa aaa aac ggc ctt tat gaa gct aaa acc aat ctt tct	344
Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser	
	85 90 95
atg aac ggg aca tgg cag gtt agg gtg gat att aaa tct aaa gag ggt	392
Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly	
	100 105 110

cag gtt tat cgc gct aaa aca agc ctg gat tta taagagcatg ctatctttta 445
 Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
 115 120 125

taagcgcggtt tgataaaagg ggcgtttcaa tac 478

<210> 220
 <211> 125
 <212> PRT
 <213> Helicobacter pylori

<400> 220
 Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
 1 5 10 15
 Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
 20 25 30
 Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
 35 40 45
 Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
 50 55 60
 Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
 65 70 75 80
 Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
 85 90 95
 Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
 100 105 110
 Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
 115 120 125

<210> 221
 <211> 1117
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1064)

<400> 221
 agcgccttta atagcactta tttgtcttta caaaacctta aaggattaga atg aaa 56
 Met Lys
 1
 cgg att tta tgg tta gcc ttg att tta ttt ttt agc ccc tta ttc gct 104
 Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu Phe Ala
 5 10 15
 aac gct caa aaa act caa gaa att aaa aaa act aaa gaa gct aaa agc 152
 Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala Lys Ser
 20 25 30
 caa acc cgt ttt aat att tcc acc act aag gtc ata gaa aaa gaa ttt 200
 Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe
 35 40 45 50

tct caa agc cgg cgc tat tac gcg ctt tta gag ccc aat gaa gcg ctg	248
Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu Ala Leu	
55 60 65	
att ttt tct caa acc ctg cgt ttt gat ggc tat gtg gaa aag ctt tat	296
Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr	
70 75 80	
gcg aat aaa acc tat acc ccc att aaa aag ggc gac agg tta ttg agc	344
Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser	
85 90 95	
gtg tat tcc cct gaa tta gtg agc gct caa agc gaa ttg cta tca tca	392
Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser	
100 105 110	
ttg aaa ttc aac caa caa gtg gga gcg att aaa gaa aaa tta aaa cta	440
Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu	
115 120 125 130	
tta ggg tta gaa aac tct agc att gaa aaa atc att agc agc cat aaa	488
Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys	
135 140 145	
gtc caa aat gaa atg act att tac tct cac ttc aac ggc att att ttt	536
Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe	
150 155 160	
aaa aaa agc ccg gat ctc aat gag ggg agc ttc att aaa aaa ggg caa	584
Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln	
165 170 175	
gag ttg ttt caa atc ata gat tta agc caa ttg tgg gcg ctg gtt aaa	632
Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys	
180 185 190	
gtc aat caa gag gat tta gaa ttt tta aaa aac acg cat aaa gcg atc	680
Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile	
195 200 205 210	
ttg ttt gta gaa ggg att aaa ggc gag caa gaa atc acg ctt gaa aat	728
Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn	
215 220 225	
atc aac ccc atc atc aac aaa gaa gat aaa atg cta gaa gcg cgc ttc	776
Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe	
230 235 240	
aat gtg cct aat gtt aaa cag att tat tac cct aac atg ttc gct caa	824
Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln	
245 250 255	
gta gaa atc ttt caa aaa cca caa aaa atg aag att ttg cct aaa gaa	872
Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu	

260	265	270	
gcg gtt ttg att aaa ggg ggg aaa gct atc gtg ttt aaa aaa gac gat			920
Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp			
275	280	285	290
ttt ggc tta agc ccg tta gaa att aaa gcc gtc cgc ttg agc gat ggg			968
Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly			
	295	300	305
agt tat gag att tta gag ggt tta aag gcg ggc gaa gaa gtc gct aat			1016
Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn			
	310	315	320
aac gct tta ttc gtg cta gac gct gac gct caa aac aat ggg gat tat			1064
Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr			
	325	330	335
tgaatgatag aaaagatcat tgatttaagc gttaaaaaca aactccttac cac			1117
<210> 222			
<211> 338			
<212> PRT			
<213> Helicobacter pylori			
<400> 222			
Met Lys Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu			
1	5	10	15
Phe Ala Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala			
	20	25	30
Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys			
	35	40	45
Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu			
	50	55	60
Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys			
	65	70	75
Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu			
	85	90	95
Leu Ser Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu			
	100	105	110
Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu			
	115	120	125
Lys Leu Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser			
	130	135	140
His Lys Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile			
	145	150	155
Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys			
	165	170	175
Gly Gln Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu			
	180	185	190
Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys			
	195	200	205
Ala Ile Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu			
	210	215	220
Glu Asn Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala			

225		230		235		240									
Arg	Phe	Asn	Val	Pro	Asn	Val	Lys	Gln	Ile	Tyr	Tyr	Pro	Asn	Met	Phe
				245					250					255	
Ala	Gln	Val	Glu	Ile	Phe	Gln	Lys	Pro	Gln	Lys	Met	Lys	Ile	Leu	Pro
				260					265					270	
Lys	Glu	Ala	Val	Leu	Ile	Lys	Gly	Gly	Lys	Ala	Ile	Val	Phe	Lys	Lys
				275					280					285	
Asp	Asp	Phe	Gly	Leu	Ser	Pro	Leu	Glu	Ile	Lys	Ala	Val	Arg	Leu	Ser
				290					295					300	
Asp	Gly	Ser	Tyr	Glu	Ile	Leu	Glu	Gly	Leu	Lys	Ala	Gly	Glu	Glu	Val
				305					310					315	
Ala	Asn	Asn	Ala	Leu	Phe	Val	Leu	Asp	Ala	Asp	Ala	Gln	Asn	Asn	Gly
				325					330					335	

Asp Tyr

<210> 223
 <211> 1249
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1196)

<400> 223
 aaaacttaga taaaataaca cgataaaacc atagtaataa agataacccc atg aga 56
 Met Arg
 1

ttt ttt tgc ttt ttc tta ttt ttt cta acc ttt tca aac gca cag ata 104
 Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile
 5 10 15

atg atg act ttt gat tct caa act aac gcc aaa ctc tcg cgc tct aac 152
 Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn
 20 25 30

gaa ca'g ctt tca gac atg ctc tat aaa ctc aat gaa agt tta aga atc 200
 Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile
 35 40 45 50

tat caa agc gtg ctt tcc aat aac caa gat caa ctc aaa gaa atc aaa 248
 Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys
 55 60 65

aaa gct aac agc acc cta aat agc caa agg cgt ttt ttt aac gcc agc 296
 Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn Ala Ser
 70 75 80

cag atc cgc ctt atg gac act gat gca cta ttg aaa caa agc gct ttg 344
 Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu
 85 90 95

gaa tta gaa aaa tta caa gct tta gaa aaa cac ata aaa aag ggc atg	392
Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys Gly Met	
100 105 110	
gaa caa gaa cgc tta ata gaa gaa tcc caa acg ctt ttt tta caa gag	440
Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu Gln Glu	
115 120 125 130	
cat tgc cct tat ttg agc ggc gtt aag aat tta gaa gag gct tca aac	488
His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala Ser Asn	
135 140 145	
gct tta gaa gtc caa gag caa aac aac gcc ctt ttc tta ctc aaa gag	536
Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu Lys Glu	
150 155 160	
cct aaa ctc gcc cgt ttg ctc tca cga ttg gat ttg atg agc gct tta	584
Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser Ala Leu	
165 170 175	
aac gcc ttg tgc gat cag gtt tta gaa aac caa gcc cat aac caa caa	632
Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn Gln Gln	
180 185 190	
tcc cat aac aaa att tta gaa tac aac gct ctt aaa aac cat gat ttt	680
Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His Asp Phe	
195 200 205 210	
caa gcc tat aaa gcc atg cgt ttg aaa aaa ttt aaa aac aag ctt caa	728
Gln Ala Tyr Lys Ala Met Arg Leu Lys Phe Lys Asn Lys Leu Gln	
215 220 225	
agt caa atc caa gcc caa gaa gac gct cta aaa acc ttt tta ccc tta	776
Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu	
230 235 240	
gaa aaa cgc ttg gaa act tta aaa acg cat ttt tta tgc gat aaa gaa	824
Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp Lys Glu	
245 250 255	
aac cta aaa tca tgc gct aaa gaa ttg cac caa cgc tac caa aac gcc	872
Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln Asn Ala	
260 265 270	
ctt ata gag cga gat aaa gaa tta aaa aac gct aaa aat aat aaa gaa	920
Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu	
275 280 285 290	
aag cat gct cta atc tta gcc aat tac gag cat act tta aaa acc ttg	968
Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu	
295 300 305	
aat ata gaa ttt tta agc gaa tta aat aag caa atg gcg ttt ttg aat	1016
Asn Ile Glu Phe Leu Ser Glu Leu Asn Lys Gln Met Ala Phe Leu Asn	
310 315 320	

gaa acc atg gcg tta aac gcc cga gtt tta gcc ctt tta gcc aaa cag 1064
 Glu Thr Met Ala Leu Asn Ala Arg Val Leu Ala Leu Leu Ala Lys Gln
 325 330 335

cat gcc aaa acg cca aag cct ttc aat ttg agc ggt ggt tta agc ggt 1112
 His Ala Lys Thr Pro Lys Pro Phe Asn Leu Ser Gly Gly Leu Ser Gly
 340 345 350

gat ttg agc ggt ggg aaa gct ctt att aaa aat atc cgc tta gat ccg 1160
 Asp Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile Arg Leu Asp Pro
 355 360 365 370

cat gga ttc cct agc ttt aaa aat ttt aag caa gag taggacaata 1206
 His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu
 375 380

tttgacaagc aaaaacaatt atagtaaaat aagagcataa ctt 1249

<210> 224
 <211> 382
 <212> PRT
 <213> Helicobacter pylori

<400> 224
 Met Arg Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala
 1 5 10 15
 Gln Ile Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg
 20 25 30
 Ser Asn Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu
 35 40 45
 Arg Ile Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu
 50 55 60
 Ile Lys Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn
 65 70 75 80
 Ala Ser Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser
 85 90 95
 Ala Leu Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys
 100 105 110
 Gly Met Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu
 115 120 125
 Gln Glu His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala
 130 135 140
 Ser Asn Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu
 145 150 155 160
 Lys Glu Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser
 165 170 175
 Ala Leu Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn
 180 185 190
 Gln Gln Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His
 195 200 205
 Asp Phe Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys
 210 215 220
 Leu Gln Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu
 225 230 235 240

Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser
85 90 95

gac aaa agc tct cgt ttt gaa act ttt atc agc att atg gat att tta 392
Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu
100 105 110

aaa gag cat aat cat gaa aat ttc tcc atc tcc acg caa gct cag 437
Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
115 120 125

taaagttttca acgagtggtta gcttttttaaat ctctttttgcc ctatacgcta tag 490

<210> 226
<211> 129
<212> PRT
<213> Helicobacter pylori

<400> 226
Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile
1 5 10 15
Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe
20 25 30
Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala
35 40 45
Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp
50 55 60
Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala
65 70 75 80
Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu
85 90 95
Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp
100 105 110
Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala
115 120 125
Gln

<210> 227
<211> 958
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(905)

<400> 227
tcgtttttgaa actttttatca gcattatgga tatttttaaaa gagcataatc atg aaa 56
Met Lys
1

att tct cca tct cca cgc aag ctc agt aaa gtt tca acg agt gtt agc 104
Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser Val Ser

5	10	15	
ttt tta atc tct ttt gcc cta tac gct ata ggg ttt ggc tat ttt tta	152		
Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr Phe Leu			
20 25 30			
ctg cgc gaa gac gcc cca gag cct tta gcg caa gcc ggg acc act aag	200		
Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr Thr Lys			
35 40 45 50			
ggt acc atg agt tta gcc agc atc aac act aat tcc aat aca aag act	248		
Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr Lys Thr			
55 60 65			
aat gct gag tcg gct aaa ccc aaa gaa gag cct aaa gaa aaa ccc aag	296		
Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys Pro Lys			
70 75 80			
aaa gaa gag cca aaa aaa gaa gaa ccc aaa aag gag gtt aca aag cct	344		
Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr Lys Pro			
85 90 95			
aaa cct aag cct aaa ccc aag cca aag cca aaa cca aaa cct aag cct	392		
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro			
100 105 110			
gaa ccc aaa cct gaa cca aaa ccc gag cct aag cct gag cct aaa gtt	440		
Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Val			
115 120 125 130			
gaa gag gtt aaa aaa gaa gag cct aaa gaa gag ccc aaa aaa gaa gaa	488		
Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys Glu Glu			
135 140 145			
gct aaa gag gaa gct aaa gaa aaa agc gct cct aaa caa gta aca act	536		
Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr			
150 155 160			
aag gat ata gtc aaa gaa aaa gac aag caa gaa gaa tcc aac aaa acc	584		
Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr			
165 170 175			
tct gag ggg gcc act tct gaa gct caa gct tat aac cca ggg gtg agc	632		
Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser			
180 185 190			
aac gaa ttt tta atg aag atc caa acc gct att tct tct aaa aac cgc	680		
Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg			
195 200 205 210			
tac cct aaa atg gcg cag att agg ggt att gag ggc gaa gtg ttg gtg	728		
Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val			
215 220 225			
agc ttt acg atc aat gct gat ggg agc gtt acg gac att aaa gtg gtc	776		

Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val
 230 235 240

aaa agc aac acc aca gat att tta aac cat gcg gct tta gaa gcc att 824
 Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile
 245 250 255

aaa agc gcg gca cat cta ttc cct aaa cca gaa gaa acc gtg cat cta 872
 Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val His Leu
 260 265 270

aaa atc cct atc gct tat agc ttg aaa gaa gac tgattagtct ttcttttagg 925
 Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp
 275 280 285

ggcgattcaa gccttaaaag ccgggtcaaa atc 958

<210> 228
 <211> 285
 <212> PRT
 <213> Helicobacter pylori

<400> 228

Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser
 1 5 10 15
 Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr
 20 25 30
 Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr
 35 40 45
 Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr
 50 55 60
 Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys
 65 70 75 80
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr
 85 90 95
 Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro
 100 105 110
 Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro
 115 120 125
 Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys
 130 135 140
 Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val
 145 150 155 160
 Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn
 165 170 175
 Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly
 180 185 190
 Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys
 195 200 205
 Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val
 210 215 220
 Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys
 225 230 235 240
 Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu
 245 250 255

Ala	Ile	Lys	Ser	Ala	Ala	His	Leu	Phe	Pro	Lys	Pro	Glu	Glu	Thr	Val
			260					265					270		
His	Leu	Lys	Ile	Pro	Ile	Ala	Tyr	Ser	Leu	Lys	Glu	Asp			
		275					280					285			

<210> 229
 <211> 757
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(704)

<400> 229 ttgatgaaaa aaataacgct cctcttttta aaactctttt agaggatgcc atg aga															56	
														Met Arg		
														1		
gtg tct tct aaa gag att tta ctc att gtg ggg ggg agc agt ttt tac															104	
Val	Ser	Ser	Lys	Glu	Ile	Leu	Leu	Ile	Val	Gly	Gly	Ser	Ser	Phe	Tyr	
		5					10					15				
ctc aaa tcc att tta gaa ggt ttg agc cgc atg cca aaa ctg agc ggt															152	
Leu	Lys	Ser	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Met	Pro	Lys	Leu	Ser	Gly	
	20					25					30					
gag gag gtt gta aaa ata gag cga gaa att gcc act ctt tct aac cct															200	
Glu	Glu	Val	Val	Lys	Ile	Glu	Arg	Glu	Ile	Ala	Thr	Leu	Ser	Asn	Pro	
	35				40				45					50		
tat ata ttt tta aaa tcc att gac cct aac atg gct ttt aaa atc cat															248	
Tyr	Ile	Phe	Leu	Lys	Ser	Ile	Asp	Pro	Asn	Met	Ala	Phe	Lys	Ile	His	
			55					60						65		
cca aac gac act tac cgc acc cat aag gct tta gaa atc ttt tat gcc															296	
Pro	Asn	Asp	Thr	Tyr	Arg	Thr	His	Lys	Ala	Leu	Glu	Ile	Phe	Tyr	Ala	
			70					75					80			
acc tgc acg ccc cca agc gag tat ttt aag gcc aac cct aaa aaa ccc															344	
Thr	Cys	Thr	Pro	Pro	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Pro	Lys	Lys	Pro	
		85				90					95					
ttt gag cat gct atc tcc tta ttc gct ctg tct att gaa aaa agc gcg															392	
Phe	Glu	His	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Ile	Glu	Lys	Ser	Ala	
	100					105					110					
ctc cat aac aat atc aaa cgg cgc acc aaa aac atg ctc cat tca ggg															440	
Leu	His	Asn	Asn	Ile	Lys	Arg	Arg	Thr	Lys	Asn	Met	Leu	His	Ser	Gly	
115				120					125					130		
ctt gtt gaa gaa atc aaa gcc ctc tat act caa tac cct aaa gat tcg															488	
Leu	Val	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Thr	Gln	Tyr	Pro	Lys	Asp	Ser	
				135				140						145		

cag cct ttt aaa gcc ata ggc gtt aaa gag agc gtt ctt ttt tta gaa 536
Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe Leu Glu
150 155 160

aaa cga ctc act tta aag gag cta gaa gaa gcg att acc tct aac acc 584
Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser Asn Thr
165 170 175

atg aaa tta gcc aag cgc caa aac act ttc aat aaa acc caa ttc aat 632
Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln Phe Asn
180 185 190

aac ctt tat gtg ggg agc gct gaa gaa gtt agg cat gcg att tta aaa 680
Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile Leu Lys
195 200 205 210

cac tca aaa agc ggc att aaa gga taatctaattg gatacacaaa acttaccgga 734
His Ser Lys Ser Gly Ile Lys Gly
215

tcaaattatc cctattttta tga 757

<210> 230
<211> 218
<212> PRT
<213> Helicobacter pylori

<400> 230
Met Arg Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser
1 5 10 15
Phe Tyr Leu Lys Ser Ile Leu Glu Gly Leu Ser Arg Met Pro Lys Leu
20 25 30
Ser Gly Glu Glu Val Val Lys Ile Glu Arg Glu Ile Ala Thr Leu Ser
35 40 45
Asn Pro Tyr Ile Phe Leu Lys Ser Ile Asp Pro Asn Met Ala Phe Lys
50 55 60
Ile His Pro Asn Asp Thr Tyr Arg Thr His Lys Ala Leu Glu Ile Phe
65 70 75 80
Tyr Ala Thr Cys Thr Pro Pro Ser Glu Tyr Phe Lys Ala Asn Pro Lys
85 90 95
Lys Pro Phe Glu His Ala Ile Ser Leu Phe Ala Leu Ser Ile Glu Lys
100 105 110
Ser Ala Leu His Asn Asn Ile Lys Arg Arg Thr Lys Asn Met Leu His
115 120 125
Ser Gly Leu Val Glu Glu Ile Lys Ala Leu Tyr Thr Gln Tyr Pro Lys
130 135 140
Asp Ser Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe
145 150 155 160
Leu Glu Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser
165 170 175
Asn Thr Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln
180 185 190
Phe Asn Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile
195 200 205

Leu Lys His Ser Lys Ser Gly Ile Lys Gly
 210 215

<210> 231
 <211> 454
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(401)

<400> 231
 ctatatgaac aaagccttaa aagacttgaa aaaaggaata actcatacct atg cga 56
 Met Arg
 1
 aac aat aaa acg cct ttt ttg agc gcg att ttt acg gca tca att agg 104
 Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg
 5 10 15
 ggt tac caa cgc ttt ttt tcg gct ttc acc cct tca agc tgc cgg ttt 152
 Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe
 20 25 30
 tac ccc act tgt tcc aac tac gct ctg tgg ttg ctc tgt ttt gaa agc 200
 Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser
 35 40 45 50
 cct ttg agc gct atg ggt aag atc gct ata agg ata ctc tca tgc aac 248
 Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn
 55 60 65
 cct ttt tgc tct ggg ggc att gct tac cct act act cgc ttg aaa cgc 296
 Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg
 70 75 80
 cca agc ctg atc caa tct cat aaa gat tct aat cgc aat ttt aaa acc 344
 Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr
 85 90 95
 atc act ttt tgg ctc gtt ccc aca aaa agc cac gca act tac tac atc 392
 Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile
 100 105 110
 att aag gtt taatcacaat ggataaaaac aacaataatc tccgcttgat 441
 Ile Lys Val
 115
 ttttagcgatc gct 454

<210> 232
 <211> 117
 <212> PRT

<213> Helicobacter pylori

<400> 232

Met	Arg	Asn	Asn	Lys	Thr	Pro	Phe	Leu	Ser	Ala	Ile	Phe	Thr	Ala	Ser	
1				5				10						15		
Ile	Arg	Gly	Tyr	Gln	Arg	Phe	Phe	Ser	Ala	Phe	Thr	Pro	Ser	Ser	Cys	
		20						25					30			
Arg	Phe	Tyr	Pro	Thr	Cys	Ser	Asn	Tyr	Ala	Leu	Trp	Leu	Leu	Cys	Phe	
		35					40					45				
Glu	Ser	Pro	Leu	Ser	Ala	Met	Gly	Lys	Ile	Ala	Ile	Arg	Ile	Leu	Ser	
	50					55					60					
Cys	Asn	Pro	Phe	Cys	Ser	Gly	Gly	Ile	Ala	Tyr	Pro	Thr	Thr	Arg	Leu	
65					70					75					80	
Lys	Arg	Pro	Ser	Leu	Ile	Gln	Ser	His	Lys	Asp	Ser	Asn	Arg	Asn	Phe	
				85					90					95		
Lys	Thr	Ile	Thr	Phe	Trp	Leu	Val	Pro	Thr	Lys	Ser	His	Ala	Thr	Tyr	
			100					105						110		
Tyr	Ile	Ile	Lys	Val												
			115													

<210> 233

<211> 1153

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1100)

<400> 233

ttataataag	aaagttttta	ttatttttaa	tgctatttta	ggagttcatc	atg	aaa	56
					Met	Lys	
					1		
aaa	tcc	att	tta	ttg	ggc	gtt	104
Lys	Ser	Ile	Leu	Leu	Gly	Val	
	5				10		
cta	aac	gat	tta	gaa	ttg	atc	152
Leu	Asn	Asp	Leu	Glu	Leu	Ile	
	20				25		
ccc	atg	cct	atg	ggc	aaa	gcg	200
Pro	Met	Pro	Met	Gly	Lys	Ala	
	35				40		
aga	gat	gtg	ggt	att	ggc	acc	248
Arg	Asp	Val	Gly	Ile	Gly	Thr	
			55				
caa	gtg	gaa	tta	ggc	aaa	atg	296
Gln	Val	Glu	Leu	Gly	Lys	Met	
			70				

tcc tac ctc gtg tct tgc aac aca tgc cat aat ctg ggc tta ggc ggg	344
Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu Gly Gly	
85 90 95	
gtg gat tta gtc cca agc gcc ata ggc tct caa tgg aag aaa aac ccc	392
Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys Asn Pro	
100 105 110	
cac ctt tta agc tcc cca acg gtg tat aac tct gtg ttt aac gat gtg	440
His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn Asp Val	
115 120 125 130	
cag ttt tgg gat ggc agg gtt acg cat tta aac gaa cag gcg caa ggg	488
Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala Gln Gly	
135 140 145	
ccc atc cag tct tct ttt gaa atg ggg gct gat ccc aaa gtg gtg gta	536
Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val Val Val	
150 155 160	
gaa aaa atc aat tcc atg cca ggc tat gtc aag ctc ttt aga aaa gcc	584
Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg Lys Ala	
165 170 175	
tat ggc tct aaa gtc aaa att gat ttt aaa ttg atc gct gat agt atc	632
Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp Ser Ile	
180 185 190	
gct atg ttt gaa gcc acg ctt att acc cca agc cgt tac gac gat ttt	680
Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp Asp Phe	
195 200 205 210	
tta aga ggc aat cct aaa gcg ctc agc aaa gcc gaa aaa gag ggg ctg	728
Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu Gly Leu	
215 220 225	
aat tta ttc att tct aaa ggc tgt gtg gct tgc cat aac ggc att aat	776
Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly Ile Asn	
230 235 240	
ctt ggg gga acg atg cag cct ttt ggg gtg gtc aaa cct tat aaa ttc	824
Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr Lys Phe	
245 250 255	
gct aat gtg ggc gat ttc aaa ggc gat aaa aac ggg ctt gtg aaa gtg	872
Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val Lys Val	
260 265 270	
cct act tta agg aat atc acc gaa acg atg ccc tat ttc cat aac ggg	920
Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His Asn Gly	
275 280 285 290	
caa ttc tgg gat gtt aag gat gcg att aaa gaa atg ggc tct atc cag	968
Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser Ile Gln	
295 300 305	

tta ggc att gaa atc agc gat gaa gaa gcg aaa aaa att gaa act ttc 1016
 Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu Thr Phe
 310 315 320

ttt gga gcc tta agg ggt aaa aaa cct aaa ata atc tac cca gaa ctc 1064
 Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro Glu Leu
 325 330 335

ccc ata atg aca gac aaa acc cct aaa ccc tct ttt tgatttaaaaa 1110
 Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe
 340 345 350

aagtcctttt aggggtcttt ggcgctaaat ctaaaaaata ctc 1153

<210> 234

<211> 350

<212> PRT

<213> Helicobacter pylori

<400> 234

Met Lys Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala
 1 5 10 15
 His Ala Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln
 20 25 30
 Leu Glu Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys
 35 40 45
 Lys Thr Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr
 50 55 60
 Ser Ala Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile
 65 70 75 80
 Ser Thr Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu
 85 90 95
 Gly Gly Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys
 100 105 110
 Asn Pro His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn
 115 120 125
 Asp Val Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala
 130 135 140
 Gln Gly Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val
 145 150 155 160
 Val Val Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg
 165 170 175
 Lys Ala Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp
 180 185 190
 Ser Ile Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp
 195 200 205
 Asp Phe Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu
 210 215 220
 Gly Leu Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly
 225 230 235 240
 Ile Asn Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr
 245 250 255
 Lys Phe Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val
 260 265 270

[illegible]

<210> 236
 <211> 108
 <212> PRT
 <213> Helicobacter pylori

<400> 236
 Met Lys Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala
 1 5 10 15
 Asn Pro Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala
 20 25 30
 Gln Phe Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala
 35 40 45
 Tyr Arg Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp
 50 55 60
 Leu Glu Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn
 65 70 75 80
 Ala Glu Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn
 85 90 95
 Ala Ser Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
 100 105

<210> 237
 <211> 799
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(746)

<400> 237
 agcgtgagcc caattacgcc acgcctatgt ctagataggg gaggttggaa atg ttt 56
 Met Phe
 1
 agt ttt tta gaa aaa aac ccg ttc ttt ttc act ctt gcg ttt att ttt 104
 Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe Ile Phe
 5 10 15
 gtg ttt gcg atc gcg ggc ttg gtg gag att ttg ccc aac ttc ttc aaa 152
 Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe Phe Lys
 20 25 30
 tcc gct cgc ccg att gaa ggc tta cgg cct tat acg gtt tta gag aca 200
 Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu Glu Thr
 35 40 45 50
 gcg ggg agg caa att tat atc caa gaa ggt tgc tat cat tgc cat tcc 248
 Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys His Ser
 55 60 65
 cag ctt att cgc cct ttc caa gct gag gtg gat cga tat ggc gcg tat 296
 Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly Ala Tyr
 70 75 80

agt ttg agt ggg gaa tac gcg tat gac agg cca ttt ttg tgg ggt tct 344
 Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp Gly Ser
 85 90 95

aaa agg att ggc cct gat ttg cac agg gta ggg gat tat cgc aca acc 392
 Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg Thr Thr
 100 105 110

gat tgg cat gaa aag cac atg ttt gat cct aaa agc gtt gtg ccg cac 440
 Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val Pro His
 115 120 125 130

agc atc atg ccc gcc tat aag cat tta ttt aca aaa aag agc gat ttt 488
 Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser Asp Phe
 135 140 145

gac acc gct tat gca gaa gct ttg acg caa aaa aag gtt ttt ggc gtg 536
 Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe Gly Val
 150 155 160

cct tat gac aca gaa aac ggc gtg aaa tta ggg agc gta gaa gaa gcg 584
 Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu Glu Ala
 165 170 175

aaa aaa gcc tat tta gaa gaa gct aaa aaa atc aca gcc gat atg aaa 632
 Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp Met Lys
 180 185 190

gac aag agg gtg cta gaa gcg att gag aga ggt gaa gtg tta gaa att 680
 Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu Glu Ile
 195 200 205 210

gtg gct ttg atc gct tat ttg aat agc ttg ggt aat tcc agg atc aac 728
 Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg Ile Asn
 215 220 225

gcc aat caa aac gct aaa taaggggtga atgatggatt tagaaagttt 776
 Ala Asn Gln Asn Ala Lys
 230

gagaggtttt gcgtatgcgt ttt 799

<210> 238
 <211> 232
 <212> PRT
 <213> *Helicobacter pylori*

<400> 238
 Met Phe Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe
 1 5 10 15
 Ile Phe Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe
 20 25 30
 Phe Lys Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu
 35 40 45

Glu	Thr	Ala	Gly	Arg	Gln	Ile	Tyr	Ile	Gln	Glu	Gly	Cys	Tyr	His	Cys	
50						55					60					
His	Ser	Gln	Leu	Ile	Arg	Pro	Phe	Gln	Ala	Glu	Val	Asp	Arg	Tyr	Gly	
65					70					75					80	
Ala	Tyr	Ser	Leu	Ser	Gly	Glu	Tyr	Ala	Tyr	Asp	Arg	Pro	Phe	Leu	Trp	
			85					90						95		
Gly	Ser	Lys	Arg	Ile	Gly	Pro	Asp	Leu	His	Arg	Val	Gly	Asp	Tyr	Arg	
			100				105						110			
Thr	Thr	Asp	Trp	His	Glu	Lys	His	Met	Phe	Asp	Pro	Lys	Ser	Val	Val	
		115					120					125				
Pro	His	Ser	Ile	Met	Pro	Ala	Tyr	Lys	His	Leu	Phe	Thr	Lys	Lys	Ser	
	130					135					140					
Asp	Phe	Asp	Thr	Ala	Tyr	Ala	Glu	Ala	Leu	Thr	Gln	Lys	Lys	Val	Phe	
145					150				155						160	
Gly	Val	Pro	Tyr	Asp	Thr	Glu	Asn	Gly	Val	Lys	Leu	Gly	Ser	Val	Glu	
				165				170						175		
Glu	Ala	Lys	Lys	Ala	Tyr	Leu	Glu	Glu	Ala	Lys	Lys	Ile	Thr	Ala	Asp	
			180					185					190			
Met	Lys	Asp	Lys	Arg	Val	Leu	Glu	Ala	Ile	Glu	Arg	Gly	Glu	Val	Leu	
		195					200					205				
Glu	Ile	Val	Ala	Leu	Ile	Ala	Tyr	Leu	Asn	Ser	Leu	Gly	Asn	Ser	Arg	
	210					215					220					
Ile	Asn	Ala	Asn	Gln	Asn	Ala	Lys									
225						230										

<210> 239
 <211> 322
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(269)

<400> 239																	
cttgggtaat	tccaggatca	acgccaatca	aaacgctaaa	taaggggtga	atg	atg										56	
					Met	Met											
					1												
gat	tta	gaa	agt	ttg	aga	ggg	ttt	gcg	tat	gcg	ttt	ttt	acc	att	ctt	104	
Asp	Leu	Glu	Ser	Leu	Arg	Gly	Phe	Ala	Tyr	Ala	Phe	Phe	Thr	Ile	Leu		
	5					10						15					
ttt	acg	ctc	ttt	ttg	tat	gcc	tat	att	ttt	agc	atg	tat	aga	aag	caa	152	
Phe	Thr	Leu	Phe	Leu	Tyr	Ala	Tyr	Ile	Phe	Ser	Met	Tyr	Arg	Lys	Gln		
	20					25					30						
aaa	aaa	ggc	att	atg	gat	tat	gag	cga	tac	gga	tac	tta	gcg	tta	aat	200	
Lys	Lys	Gly	Ile	Met	Asp	Tyr	Glu	Arg	Tyr	Gly	Tyr	Leu	Ala	Leu	Asn		
	35				40					45					50		
gat	gct	tta	gaa	gac	gag	ttg	att	gaa	cca	cgc	cat	aaa	aaa	gtt	cat	248	
Asp	Ala	Leu	Glu	Asp	Glu	Leu	Ile	Glu	Pro	Arg	His	Lys	Lys	Val	His		
				55				60						65			

gat aat ggc ata aag gaa agt tgaaatggat tttttaaacg accatataaa 299
 Asp Asn Gly Ile Lys Glu Ser
 70

tgtttttggc ttgattgcag cgc 322

<210> 240
 <211> 73
 <212> PRT
 <213> Helicobacter pylori

<400> 240
 Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
 1 5 10 15
 Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
 20 25 30
 Lys Gln Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
 35 40 45
 Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys
 50 55 60
 Val His Asp Asn Gly Ile Lys Glu Ser
 65 70

<210> 241
 <211> 1021
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(968)

<400> 241
 ttactgattt ttctttgtgt gagctttggc ttagttttgt aaggaatgag atg ata 56
 Met Ile
 1
 aag agt tgg act aaa aag tgg ttt ttg att tta ttt tta atg gca agt 104
 Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser
 5 10 15
 tgt tcc agt tat ttg gtg gct aca acc ggt gag aaa tat ttt aaa atg 152
 Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met
 20 25 30
 gct act caa gcc ttt aag aga ggg gac tac cat aaa gcg gtg gct ttt 200
 Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe
 35 40 45 50
 tat aag agg agc tgt aat tta agg gtg ggg gtt ggt tgc acg agt tta 248
 Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu
 55 60 65

ggc tct atg tat gaa gat ggc gat ggc gtg gat cag aat att aca aaa	296
Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys	
70 75 80	
gcc gtt ttt tat tac aga aga ggg tgt aat tta agg aat cat ctc gct	344
Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala	
85 90 95	
tgc gcg agt cta ggc tct atg tat gaa gat ggc gat ggt gtg caa aaa	392
Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys	
100 105 110	
aac ctt cca aag gct atc tat tat tac agg aga ggg tgc cac tta aag	440
Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys	
115 120 125 130	
ggg ggt ggt ggc agc tgt ggc agt tta ggt ttt atg tat ttt aat ggc acg	488
Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr	
135 140 145	
ggc gtt aag caa aat tat gcc aaa gcc ctt ttt ctt tct aaa tac gct	536
Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala	
150 155 160	
tgc agt ttg aat tac ggc att agt tgt aac ttt gta ggg tat atg tat	584
Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr	
165 170 175	
agg aac gcc aaa ggc gta cag aag gat ttg aaa aaa gcc ctt gcg aat	632
Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn	
180 185 190	
ttt aaa aga ggg tgc cat ttg aaa gac gga gcg agt tgt gtg agc ttg	680
Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu	
195 200 205 210	
gga tac atg tat gaa gtc ggt atg gat gtc aaa caa aat gga gag caa	728
Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln	
215 220 225	
gcc ttg aat ctt tat aaa aag ggt tgt tat tta aaa agg ggg agc ggt	776
Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly	
230 235 240	
tgt cat aat gtg gcg gtg atg tat tac acc ggt aag ggc gtt cca aag	824
Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys	
245 250 255	
gat tta gat aaa gcc att tcg tat tat aag aaa ggt tgc act cta ggc	872
Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly	
260 265 270	
ttt agt ggt agc tgt aaa gtg tta gaa gaa gtg att ggc aag aag tct	920
Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser	
275 280 285 290	

gat gat ttg caa gat gac gcg caa aac gac acg caa gat gat atg caa 968
 Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln
 295 300 305

taagttaaag cttatggact aatgattaaa actcatctta tagaaatctt tct 1021

<210> 242

<211> 306

<212> PRT

<213> Helicobacter pylori

<400> 242

Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
 1 5 10 15
 Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
 20 25 30
 Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val
 35 40 45
 Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr
 50 55 60
 Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile
 65 70 75 80
 Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
 85 90 95
 Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
 100 105 110
 Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
 115 120 125
 Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
 130 135 140
 Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys
 145 150 155 160
 Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
 165 170 175
 Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu
 180 185 190
 Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
 195 200 205
 Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly
 210 215 220
 Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly
 225 230 235 240
 Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val
 245 250 255
 Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr
 260 265 270
 Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys
 275 280 285
 Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp
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 Met Gln
 305

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-305-

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 Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu Ala Asn
 180 185 190
 cgg gat acg att gat cct aac agc aag aac gcg caa aat ggc ggt gat 680
 Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly Gly Asp
 195 200 205 210
 ttg ggg aaa ttc caa aag aac caa atg gct ccg gat ttt tct aaa gcc 728
 Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser Lys Ala
 215 220 225
 gct ttc gct tta act cct ggg gat tac act aaa acc cct gtt aaa aca 776
 Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val Lys Thr
 230 235 240
 gag ttt ggt tat cat att atc tat ttg att tct aaa gat agc cct gta 824
 Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser Pro Val
 245 250 255
 act tat act tat gaa cag gct aaa cct acc att aag ggg atg tta caa 872
 Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln
 260 265 270
 gaa aag ctt ttc caa gaa cgc atg aat caa cgc att gag gaa cta aga 920
 Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg
 275 280 285 290
 aag cac gct aaa att gtt atc aac aag taattgatga ggtggttatca 967
 Lys His Ala Lys Ile Val Ile Asn Lys
 295
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 Asn Thr Lys Lys Thr Thr Asp Ser Ala Gly Val Leu Ala Thr Val
 35 40 45
 Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
 50 55 60
 Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
 65 70 75 80
 Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
 85 90 95

Thr	Glu	Lys	Leu	Asp	Ser	Thr	Pro	Glu	Phe	Lys	Ala	Met	Met	Glu	Ala		
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Val	Lys	Lys	Gln	Ala	Leu	Val	Glu	Phe	Trp	Ala	Lys	Lys	Gln	Ala	Glu		
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Glu	Val	Lys	Lys	Val	Gln	Ile	Pro	Glu	Lys	Glu	Met	Gln	Asp	Phe	Tyr		
		130				135					140						
Asn	Ala	Asn	Lys	Asp	Gln	Leu	Phe	Val	Lys	Gln	Glu	Ala	His	Ala	Arg		
145					150					155					160		
His	Ile	Leu	Val	Lys	Thr	Glu	Asp	Glu	Ala	Lys	Arg	Ile	Ile	Ser	Glu		
			165						170					175			
Ile	Asp	Lys	Gln	Pro	Lys	Ala	Lys	Lys	Glu	Ala	Lys	Phe	Ile	Glu	Leu		
		180						185					190				
Ala	Asn	Arg	Asp	Thr	Ile	Asp	Pro	Asn	Ser	Lys	Asn	Ala	Gln	Asn	Gly		
		195					200					205					
Gly	Asp	Leu	Gly	Lys	Phe	Gln	Lys	Asn	Gln	Met	Ala	Pro	Asp	Phe	Ser		
	210					215					220						
Lys	Ala	Ala	Phe	Ala	Leu	Thr	Pro	Gly	Asp	Tyr	Thr	Lys	Thr	Pro	Val		
225					230					235					240		
Lys	Thr	Glu	Phe	Gly	Tyr	His	Ile	Ile	Tyr	Leu	Ile	Ser	Lys	Asp	Ser		
			245						250					255			
Pro	Val	Thr	Tyr	Thr	Tyr	Glu	Gln	Ala	Lys	Pro	Thr	Ile	Lys	Gly	Met		
		260						265					270				
Leu	Gln	Glu	Lys	Leu	Phe	Gln	Glu	Arg	Met	Asn	Gln	Arg	Ile	Glu	Glu		
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<211> 376

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (51)...(323)

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Lys	Val	Val	Phe	Leu	Leu	Leu	Val	Ile	Leu	Gly	Gly	Leu	Glu	Ala	Gln	
		5					10					15				

agt	act	tat	tgc	agt	gat	cat	tgc	gaa	ggc	acg	cca	gat	agc	cgt	atc	152
Ser	Thr	Tyr	Cys	Ser	Asp	His	Cys	Glu	Gly	Thr	Pro	Asp	Ser	Arg	Ile	
		20				25					30					

cct	cct	atg	ggg	ttt	cat	ttc	agt	ttt	gtg	cat	tca	gtg	aaa	tat	tac	200
Pro	Pro	Met	Gly	Phe	His	Phe	Ser	Phe	Val	His	Ser	Val	Lys	Tyr	Tyr	
	35				40				45					50		

ttg	caa	gat	ccg	caa	gag	cgc	gat	cac	aag	ctt	gaa	aaa	tgc	cat	caa	248
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

gaa aga gtg att tac ttg gct ggg ggg tgt ttt tgg ggg cta gag gcg	200
Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu Glu Ala	
35 40 45 50	
tat atg gag agg att tat ggc gtc ata gac gca agc tct ggt tac gct	248
Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala	
55 60 65	
aac ggc aag act tca agc acg aat tat gag aaa ttg cat gaa agt gat	296
Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu Ser Asp	
70 75 80	
cat gct gaa agc gtg aaa gtc att tat gat cct aaa aaa atc agt ttg	344
His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu	
85 90 95	
gac aaa ttg ttg cgt tac tat ttt aag gtg gtt gat ccg gtg agc gtg	392
Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val Ser Val	
100 105 110	
aac aag cag ggt aat gat gtg ggc agg cag tat cgc acg ggg att tat	440
Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr	
115 120 125 130	
tat gtc aat agc gcg gat aaa gaa gtg ata gat cat gcc tta aaa gcg	488
Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu Lys Ala	
135 140 145	
tta cag aaa gaa gtg aaa ggt aaa atc gct att gaa gta gag cct tta	536
Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu Pro Leu	
150 155 160	
aaa aat tat gtg agg gct gaa gag tat cat cag gat tat ttg aag aaa	584
Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu Lys Lys	
165 170 175	
cac cct agt ggt tat tgc cat att gat ttg aaa aag gcg gat gaa gtg	632
His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp Glu Val	
180 185 190	
att gtg gat gac gat aaa tac acc aaa cct agc gat gaa gtt tta aag	680
Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val Leu Lys	
195 200 205 210	
aaa aaa ctc acc aaa ctc cag tat gag gtt acg caa aac aaa cac act	728
Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys His Thr	
215 220 225	
gag aaa ccc ttt gaa aac gag tat tac aac aaa gaa gaa gag ggc att	776
Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu Gly Ile	
230 235 240	
tat gtg gat att acc aca ggc gag ccg tta ttt tct tca gcg gat aaa	824
Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala Asp Lys	
245 250 255	

tac gac tcc ggt tgc ggg tgg cca agc ttt tct aag cct atc aat aaa 872
 Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile Asn Lys
 260 265 270

gat gtg gtg aaa tac gaa gac gat gag agc ctt aat agg aaa cgc att 920
 Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys Arg Ile
 275 280 285 290

gaa gtg ttg agc cgt att ggt aag gcg cat tta ggg cat gtg ttt aac 968
 Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val Phe Asn
 295 300 305

gat ggg cct aaa gaa tta ggg ggc tta agg tat tgc atc aac agc gcg 1016
 Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn Ser Ala
 310 315 320

gct tta agg ttt atc ccc tta aaa gac atg gaa aaa gag ggt tat ggc 1064
 Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly Tyr Gly
 325 330 335

gag ttt atc cct tat atc aaa aag ggt gaa ttg aaa aaa tac atc aat 1112
 Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr Ile Asn
 340 345 350

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 Thr Asp Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu
 35 40 45
 Glu Ala Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly
 50 55 60
 Tyr Ala Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu
 65 70 75 80
 Ser Asp His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile
 85 90 95
 Ser Leu Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val
 100 105 110
 Ser Val Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly
 115 120 125
 Ile Tyr Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu
 130 135 140

Lys Ala Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu
 145 150 155 160
 Pro Leu Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu
 165 170 175
 Lys Lys His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp
 180 185 190
 Glu Val Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val
 195 200 205
 Leu Lys Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys
 210 215 220
 His Thr Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu
 225 230 235 240
 Gly Ile Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala
 245 250 255
 Asp Lys Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile
 260 265 270
 Asn Lys Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys
 275 280 285
 Arg Ile Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val
 290 295 300
 Phe Asn Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn
 305 310 315 320
 Ser Ala Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly
 325 330 335
 Tyr Gly Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr
 340 345 350
 Ile Asn Asp Lys Lys Ser His
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<220>
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 Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu Gly Ala
 5 10 15

 gcc cct aaa cat tca gtt tca gct aat gac aaa cgg atg cag gat aat 152
 Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln Asp Asn
 20 25 30

 tta gtg agc gtg att gaa aaa cag acc aat aaa aag gtg cgt att tta 200
 Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg Ile Leu
 35 40 45 50

gaa atc aaa cct tta aaa tct agc cag gat tta aaa atg gtc gtt att	248
Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val Val Ile	
55 60 65	
gaa gat ccg gac act aaa tac aat atc ccg ctt gtg gtg agt aag gat	296
Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser Lys Asp	
70 75 80	
ggg aat tta atc ata ggg ctt agc aac ata ttc ttt agc aat aaa agc	344
Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn Lys Ser	
85 90 95	
gat gat gtg caa tta gtt gca gaa acc aat caa aaa gtt caa gct ctt	392
Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln Ala Leu	
100 105 110	
aac gcc acc caa caa aat agc gcg aaa ttg aac gct att ttt aat gaa	440
Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe Asn Glu	
115 120 125 130	
ata ccg gct gat tat gcg ata gag ttg ccc tct act aac gct gca aat	488
Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala Ala Asn	
135 140 145	
aag gat aaa atc ctt tat att gtc tct gat ccc atg tgc cca cat tgc	536
Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro His Cys	
150 155 160	
caa aaa gag ctc act aaa ctt agg gat cat tta aaa gaa aac acc gtg	584
Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn Thr Val	
165 170 175	
aga atg gtc gtg gtg ggg tgg ctt ggg gtc aat tca gct aaa aaa gcg	632
Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys Lys Ala	
180 185 190	
gct tta atc caa gaa gaa atg gcg aaa gct agg gct agg gga gcg agc	680
Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly Ala Ser	
195 200 205 210	
gtg gaa gat aag atc tct att ctt gaa aag att tat tcc acc caa tac	728
Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr Gln Tyr	
215 220 225	
gat att aac gct caa aaa gag cct gaa gat tta cgc act aaa gtg gaa	776
Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys Val Glu	
230 235 240	
aat acc act aaa aag att ttt gaa tct ggc gtg att aag ggt gtg cct	824
Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly Val Pro	
245 250 255	
ttc tta tac cat tat aag gca tgatataagg ttgctctcat gaaaaaaccc	875
Phe Leu Tyr His Tyr Lys Ala	

260

265

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898

<210> 250

<211> 265

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<213> Helicobacter pylori

<400> 250

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Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
 35           40           45
Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
 50           55           60
Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
 65           70           75           80
Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
 85           90           95
Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
100           105           110
Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe
115           120           125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala
130           135           140
Ala Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro
145           150           155           160
His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn
165           170           175
Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys
180           185           190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
195           200           205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
210           215           220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
225           230           235           240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
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Val Pro Phe Leu Tyr His Tyr Lys Ala
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<211> 760

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(707)

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gcc gcg caa gaa ttg ttg caa tgc tct gcg att ttt gaa tct aaa aaa	152
Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys	
20 25 30	
gcc gaa ttg aaa gac gat ttg cgc cga ttg agt gaa aaa gag cag tct	200
Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser	
35 40 45 50	
tta agg atc ttg caa acc gaa aac gcc gcg ctt tta gat gaa aaa acc	248
Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Thr	
55 60 65	
gat ctg ttg aac caa aaa gaa aaa gaa gtg gaa gaa aaa ctg aaa aat	296
Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn	
70 75 80	
tta gcc gct aaa gaa gaa gcc ttt aaa acc tta caa acg gaa gaa aaa	344
Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys	
85 90 95	
aaa cgc ctt aaa aat ttg ata gaa gaa aac gaa ggc att tta aga gaa	392
Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu	
100 105 110	
atc aag cag gct aaa gac agc aag att ggc gag act tat tct aaa atg	440
Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met	
115 120 125 130	
aaa gat tct aaa tcg gct ctg att tta gaa aat tta ccc act caa aac	488
Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn	
135 140 145	
gca tta gaa att tta atg gcg cta aaa ccc caa gaa ctc ggt aaa att	536
Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile	
150 155 160	
tta gcc aaa atg gat cct aaa aaa gcg gcg gct ttg aca gag ttg tgg	584
Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu Leu Trp	
165 170 175	
caa aaa ccc cca aaa gaa aat aaa gaa atc cca aaa acc aca gca ccc	632
Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr Ala Pro	
180 185 190	
acg ccc cct ata gca ccc acg cct tta aaa gag ccg atg ata aaa gat	680
Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile Lys Asp	

195 200 205 210

cct aac acc aaa gag cct gca ggg gta tgatgttcat tgtagcgggt 727

Pro Asn Thr Lys Glu Pro Ala Gly Val

215

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<211> 219

<212> PRT

<213> *Helicobacter pylori*

<400> 252

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			20					25					30		
Lys	Lys	Ala	Glu	Leu	Lys	Asp	Asp	Leu	Arg	Arg	Leu	Ser	Glu	Lys	Glu
		35				40					45				
Gln	Ser	Leu	Arg	Ile	Leu	Gln	Thr	Glu	Asn	Ala	Arg	Leu	Leu	Asp	Glu
	50				55				60						
Lys	Thr	Asp	Leu	Leu	Asn	Gln	Lys	Glu	Lys	Glu	Val	Glu	Glu	Lys	Leu
65				70				75						80	
Lys	Asn	Leu	Ala	Ala	Lys	Glu	Glu	Ala	Phe	Lys	Thr	Leu	Gln	Thr	Glu
			85					90					95		
Glu	Lys	Lys	Arg	Leu	Lys	Asn	Leu	Ile	Glu	Glu	Asn	Glu	Gly	Ile	Leu
			100				105					110			
Arg	Glu	Ile	Lys	Gln	Ala	Lys	Asp	Ser	Lys	Ile	Gly	Glu	Thr	Tyr	Ser
	115					120					125				
Lys	Met	Lys	Asp	Ser	Lys	Ser	Ala	Leu	Ile	Leu	Glu	Asn	Leu	Pro	Thr
	130				135					140					
Gln	Asn	Ala	Leu	Glu	Ile	Leu	Met	Ala	Leu	Lys	Pro	Gln	Glu	Leu	Gly
145				150				155						160	
Lys	Ile	Leu	Ala	Lys	Met	Asp	Pro	Lys	Lys	Ala	Ala	Ala	Leu	Thr	Glu
			165					170						175	
Leu	Trp	Gln	Lys	Pro	Pro	Lys	Glu	Asn	Lys	Glu	Ile	Pro	Lys	Thr	Thr
			180				185					190			
Ala	Pro	Thr	Pro	Pro	Ile	Ala	Pro	Thr	Pro	Leu	Lys	Glu	Pro	Met	Ile
	195					200						205			
Lys	Asp	Pro	Asn	Thr	Lys	Glu	Pro	Ala	Gly	Val					
	210					215									

<210> 253

<211> 1393

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (51) ... (1340)

<400> 253

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Ile	Gln	Ile	Lys	Lys	Arg	Phe	Leu	Ala	Asn	Leu	Leu	Leu	Phe	Ser	Leu	
5				10				15								
ttt	tgc	ctt	aag	gct	gaa	acc	ctt	tca	gaa	gat	cat	caa	atc	ctg	ttg	152
Phe	Cys	Leu	Lys	Ala	Glu	Thr	Leu	Ser	Glu	Asp	His	Gln	Ile	Leu	Leu	
20				25				30								
agt	tca	gac	gct	ttc	cat	aga	ggg	gat	ttt	gct	gcc	gct	caa	aaa	ggc	200
Ser	Ser	Asp	Ala	Phe	His	Arg	Gly	Asp	Phe	Ala	Ala	Ala	Gln	Lys	Gly	
35				40				45				50				
tat	atg	aat	ctc	tat	aag	caa	acc	aat	aag	gtg	gtg	tat	gct	aaa	gaa	248
Tyr	Met	Asn	Leu	Tyr	Lys	Gln	Thr	Asn	Lys	Val	Val	Tyr	Ala	Lys	Glu	
55				60				65								
gcg	gcc	att	tca	gcg	gcg	agc	tta	ggg	gat	att	aaa	acc	gct	atg	cat	296
Ala	Ala	Ile	Ser	Ala	Ala	Ser	Leu	Gly	Asp	Ile	Lys	Thr	Ala	Met	His	
70				75				80								
tta	gcc	atg	ctc	tat	caa	aaa	atc	acc	aat	aat	cgt	aat	gat	gtt	tct	344
Leu	Ala	Met	Leu	Tyr	Gln	Lys	Ile	Thr	Asn	Asn	Arg	Asn	Asp	Val	Ser	
85				90				95								
atc	aat	aag	att	tta	gtg	gat	ggc	tat	gcg	caa	atg	ggg	cag	att	gat	392
Ile	Asn	Lys	Ile	Leu	Val	Asp	Gly	Tyr	Ala	Gln	Met	Gly	Gln	Ile	Asp	
100				105				110								
aag	gcg	att	gaa	ttg	ctg	cac	aaa	atc	cgt	aaa	gaa	gaa	aag	acc	ata	440
Lys	Ala	Ile	Glu	Leu	Leu	His	Lys	Ile	Arg	Lys	Glu	Glu	Lys	Thr	Ile	
115				120				125				130				
gcc	aca	gac	aat	gtg	tta	ggg	act	ttg	tat	ttg	act	caa	aag	cgt	ttg	488
Ala	Thr	Asp	Asn	Val	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Gln	Lys	Arg	Leu	
135				140				145								
gat	aag	gct	ttc	cca	ttg	ttg	aat	aag	ttt	tat	aac	caa	gtg	cat	gat	536
Asp	Lys	Ala	Phe	Pro	Leu	Leu	Asn	Lys	Phe	Tyr	Asn	Gln	Val	His	Asp	
150				155				160								
gaa	gac	agc	cta	gaa	aaa	ctc	att	acg	atc	tat	ttt	ttg	caa	aat	cgt	584
Glu	Asp	Ser	Leu	Glu	Lys	Leu	Ile	Thr	Ile	Tyr	Phe	Leu	Gln	Asn	Arg	
165				170				175								
aaa	aaa	gag	ggc	ttg	gat	ttg	ttg	caa	tct	cat	ata	gac	agg	tat	ggc	632
Lys	Lys	Glu	Gly	Leu	Asp	Leu	Leu	Gln	Ser	His	Ile	Asp	Arg	Tyr	Gly	
180				185				190								
tgc	tca	gag	caa	ttg	tgc	caa	aaa	gcg	ctc	aac	act	ttc	acg	caa	ttt	680
Cys	Ser	Glu	Gln	Leu	Cys	Gln	Lys	Ala	Leu	Asn	Thr	Phe	Thr	Gln	Phe	
195				200				205				210				

aac gag ctt gat ttg gct aaa acg act ttt gct cgt ttg tat gaa aaa	728
Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr Glu Lys	
215 220 225	
aac cct att gtt caa aat gct cag ttt tac ata ggg gta tta atc ttg	776
Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu Ile Leu	
230 235 240	
tta aaa gag ttt gat aag gcc cag aaa atc gca gaa tta ttc cct ttt	824
Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe Pro Phe	
245 250 255	
gac agg cgt ttg ttg tta gac tta tac acc gca caa aaa aaa ttc gat	872
Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys Phe Asp	
260 265 270	
caa gct tcc aaa caa gct tct ttg atc tat caa gaa aaa aaa gac cct	920
Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys Asp Pro	
275 280 285 290	
aaa ttc tta gga tta gag gcc att tat cat tat gaa agc ttg agt gcg	968
Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu Ser Ala	
295 300 305	
aat aag aaa aag ctc acc aaa gaa gag atg ttg cct atc att caa aaa	1016
Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile Gln Lys	
310 315 320	
tta gag caa gcc acc aaa gag cgc caa gca tgg ctc gct aaa acc aaa	1064
Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys Thr Lys	
325 330 335	
gat aaa gaa gac gcg caa gac gct ttc ttt tat aat ttt tta ggg tat	1112
Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu Gly Tyr	
340 345 350	
tcc tta ata gat tat gac atg gat att aaa agg ggc atg gat ttt gtg	1160
Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp Phe Val	
355 360 365 370	
agg aaa gcc tta gcg ttg gat tct gga tca gtg ctt tat ttg gat tct	1208
Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu Asp Ser	
375 380 385	
tta gca tgg ggt tat tac aaa tta ggg aat tgt ttg gaa gct aaa aaa	1256
Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys	
390 395 400	
atc ttt tct agc atc gct aaa gag tct atc caa gcc gaa cct gaa ttg	1304
Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro Glu Leu	
405 410 415	
aaa gaa cac aat aaa atc att caa gaa tgc aag aaa tagggatttt	1350
Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys	
420 425 430	

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1393

<210> 254

<211> 430

<212> PRT

<213> Helicobacter pylori

<400> 254

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Ser	Leu	Phe	Cys	Leu	Lys	Ala	Glu	Thr	Leu	Ser	Glu	Asp	His	Gln	Ile
			20					25					30		
Leu	Leu	Ser	Ser	Asp	Ala	Phe	His	Arg	Gly	Asp	Phe	Ala	Ala	Ala	Gln
			35					40				45			
Lys	Gly	Tyr	Met	Asn	Leu	Tyr	Lys	Gln	Thr	Asn	Lys	Val	Val	Tyr	Ala
	50					55					60				
Lys	Glu	Ala	Ala	Ile	Ser	Ala	Ala	Ser	Leu	Gly	Asp	Ile	Lys	Thr	Ala
65					70					75					80
Met	His	Leu	Ala	Met	Leu	Tyr	Gln	Lys	Ile	Thr	Asn	Asn	Arg	Asn	Asp
				85					90					95	
Val	Ser	Ile	Asn	Lys	Ile	Leu	Val	Asp	Gly	Tyr	Ala	Gln	Met	Gly	Gln
			100					105					110		
Ile	Asp	Lys	Ala	Ile	Glu	Leu	Leu	His	Lys	Ile	Arg	Lys	Glu	Glu	Lys
		115					120					125			
Thr	Ile	Ala	Thr	Asp	Asn	Val	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Gln	Lys
	130					135					140				
Arg	Leu	Asp	Lys	Ala	Phe	Pro	Leu	Leu	Asn	Lys	Phe	Tyr	Asn	Gln	Val
145					150					155					160
His	Asp	Glu	Asp	Ser	Leu	Glu	Lys	Leu	Ile	Thr	Ile	Tyr	Phe	Leu	Gln
				165					170					175	
Asn	Arg	Lys	Lys	Glu	Gly	Leu	Asp	Leu	Leu	Gln	Ser	His	Ile	Asp	Arg
			180					185					190		
Tyr	Gly	Cys	Ser	Glu	Gln	Leu	Cys	Gln	Lys	Ala	Leu	Asn	Thr	Phe	Thr
		195					200					205			
Gln	Phe	Asn	Glu	Leu	Asp	Leu	Ala	Lys	Thr	Thr	Phe	Ala	Arg	Leu	Tyr
	210					215					220				
Glu	Lys	Asn	Pro	Ile	Val	Gln	Asn	Ala	Gln	Phe	Tyr	Ile	Gly	Val	Leu
225					230					235					240
Ile	Leu	Leu	Lys	Glu	Phe	Asp	Lys	Ala	Gln	Lys	Ile	Ala	Glu	Leu	Phe
			245						250					255	
Pro	Phe	Asp	Arg	Arg	Leu	Leu	Leu	Asp	Leu	Tyr	Thr	Ala	Gln	Lys	Lys
			260					265					270		
Phe	Asp	Gln	Ala	Ser	Lys	Gln	Ala	Ser	Leu	Ile	Tyr	Gln	Glu	Lys	Lys
		275					280					285			
Asp	Pro	Lys	Phe	Leu	Gly	Leu	Glu	Ala	Ile	Tyr	His	Tyr	Glu	Ser	Leu
	290					295					300				
Ser	Ala	Asn	Lys	Lys	Lys	Leu	Thr	Lys	Glu	Glu	Met	Leu	Pro	Ile	Ile
305					310					315					320
Gln	Lys	Leu	Glu	Gln	Ala	Thr	Lys	Glu	Arg	Gln	Ala	Trp	Leu	Ala	Lys
			325						330					335	
Thr	Lys	Asp	Lys	Glu	Asp	Ala	Gln	Asp	Ala	Phe	Phe	Tyr	Asn	Phe	Leu
			340					345					350		
Gly	Tyr	Ser	Leu	Ile	Asp	Tyr	Asp	Met	Asp	Ile	Lys	Arg	Gly	Met	Asp
		355					360						365		

Phe Val Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu
 370 375 380
 Asp Ser Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala
 385 390 395 400
 Lys Lys Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro
 405 410 415
 Glu Leu Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
 420 425 430

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 <212> DNA
 <213> *Helicobacter pylori*

<220>
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 aga ttt gtt ttg ttt tta ttg ttc atg tgc gtt tgc gtt caa gct tac 104
 Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr
 5 10 15

 gcc gag caa gat tac ttt ttt agg gat ttt aaa tct aga gat ttg ccc 152
 Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro
 20 25 30

 caa aaa ctc cat ctt gat aaa aag ctc tcc caa aca ata cag cca tgc 200
 Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys
 35 40 45 50

 atg caa ctt aac gca tca aaa cac tac act tct acc ggg gtt aga gag 248
 Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu
 55 60 65

 cct gat aaa tgc aca aag agt ttt aaa aaa tcc gct ctc atg tcc tat 296
 Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr
 70 75 80

 gac tta gcg cta ggt tat ttg gtg agt aag aat aag caa tac ggc tta 344
 Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu
 85 90 95

 aag gct ata gaa att tta aac gct tgg gct aaa gag ctt caa agc gtg 392
 Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val
 100 105 110

gat act tat cag agc gag gat aat atc aat ttt tac atg cct tat atg	440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met	
115 120 125 130	
aac atg gct tat tgg ttt gtc aaa aag gcg ttt cct agc cca gaa tat	488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr	
135 140 145	
gaa gat ttc att aag cgg atg cgc cag tat tct caa tca gct ctt aac	536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn	
150 155 160	
act aac cat ggg gcg tgg ggc att ctt ttt gat gtg agt tct gcg cta	584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu	
165 170 175	
gcg tta gac gat aat gcc ctt ttg cac aat agc gct aat cgg tgg cag	632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln	
180 185 190	
gag tgg gtg ttt aaa gcc ata gat gag aat ggg gtt att gnt agc gcg	680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala	
195 200 205 210	
atc act agg agc gat acg agc gat tat cat gcc gcc cct aca aag gcc	728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly	
215 220 225	
att aag ggg ata gct tat acc aat ttc gcg ctt ctt gcg cta acc ata	776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile	
230 235 240	
tca gcc gaa ttg ctt ttt gag aac ggg tat gat ttg tgg ggt agt gga	824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly	
245 250 255	
gct ggg aaa agg ctc tct gtg gcg tat aac aaa gtt gca aca tgg att	872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile	
260 265 270	
tta aac cct gaa act ttc cct tat ttc cag cct aac ctt atc ggg gtg	920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val	
275 280 285 290	
cat aac aac gcc tat ttc att att tta gcc aag cat tat tct agc cct	968
His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser Ser Pro	
295 300 305	
agt gca aat gag ctt tta aag caa gcc gat tta cac gaa gat ggt ttc	1016
Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp Gly Phe	
310 315 320	
agg ctg aaa ctc cga tcg cca tgaatttttc tgtatccaag gttagcctta	1067
Arg Leu Lys Leu Arg Ser Pro	

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1090

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<211> 329

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 208

<223> Xaa = Any Amino Acid

<400> 256

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Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp
			20					25					30		
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln
		35				40						45			
Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val
	50				55						60				
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met
65					70				75					80	
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr
			85					90						95	
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln
		100					105						110		
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro
	115					120					125				
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro
	130				135						140				
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala
145					150				155						160
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser
			165				170							175	
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg
		180					185						190		
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Xaa
	195					200						205			
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr
	210				215					220					
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu
225				230					235					240	
Thr	Ile	Ser	Gly	Glu	Leu	Leu	Phe	Glu	Asn	Gly	Tyr	Asp	Leu	Trp	Gly
			245					250						255	
Ser	Gly	Ala	Gly	Lys	Arg	Leu	Ser	Val	Ala	Tyr	Asn	Lys	Val	Ala	Thr
		260					265						270		
Trp	Ile	Leu	Asn	Pro	Glu	Thr	Phe	Pro	Tyr	Phe	Gln	Pro	Asn	Leu	Ile
	275					280						285			
Gly	Val	His	Asn	Asn	Ala	Tyr	Phe	Ile	Ile	Leu	Ala	Lys	His	Tyr	Ser
	290				295						300				
Ser	Pro	Ser	Ala	Asn	Glu	Leu	Leu	Lys	Gln	Gly	Asp	Leu	His	Glu	Asp
305					310					315					320

Gly Phe Arg Leu Lys Leu Arg Ser Pro
325

<210> 257
<211> 373
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (51)...(320)

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Val Asn
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ttt ttg aaa aag cca aag tat tat aaa ttc ata gag ggg gcg aat tat 104
Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala Asn Tyr
5 10 15

ttg agc ttg ggg ctt tct atg gtg gta gcg atc ctt atg ggc gtg gct 152
Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly Val Ala
20 25 30

ata ggc tat ggg ctt aaa aaa ctc act cat att tcg tgg ctt ttt tgg 200
Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu Phe Trp
35 40 45 50

ctt ggg gtt att tgg ggc gtc tta gcg agc ttt ctc aat gtc tat aaa 248
Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val Tyr Lys
55 60 65

gct tat aaa aac atg caa aaa gac tat gaa gaa cta gcc aaa gac cct 296
Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys Asp Pro
70 75 80

aaa tac aca caa aat aaa aca aaa taaatccaat caaatcccat gtgccaaatc 350
Lys Tyr Thr Gln Asn Lys Thr Lys
85 90

caatgcttgc ttattttact ttc 373

<210> 258
<211> 90
<212> PRT
<213> Helicobacter pylori

<400> 258
Val Asn Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala
1 5 10 15
Asn Tyr Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly
20 25 30
Val Ala Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu

gat gat aag atc gtg ttt tta ggc tca gcg aat tgg agc aaa aac gct 488
 Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys Asn Ala
 135 140 145

ttt gaa aac aat tat gaa gtg ctt tta aaa acc gat gac aca gaa acg 536
 Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr Glu Thr
 150 155 160

atc ctc aaa gcc aag agc tat tac caa aag atg tta ggg agt tgc gtt 584
 Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser Cys Val
 165 170 175

ggg ttt taaaagccct ttagaagtgg taattataacc ccacataaaa ggcaaagacc 640
 Gly Phe
 180

cta 643

<210> 260
 <211> 180
 <212> PRT
 <213> Helicobacter pylori

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 Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr
 20 25 30
 Glu Gln Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala
 35 40 45
 Arg Glu Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile
 50 55 60
 Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile
 65 70 75 80
 Ile Tyr Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly
 85 90 95
 Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu
 100 105 110
 Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala
 115 120 125
 Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys
 130 135 140
 Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr
 145 150 155 160
 Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser
 165 170 175
 Cys Val Gly Phe
 180

<210> 261
 <211> 814
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(761)

<400> 261

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Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe Ser Met
      5                      10                      15

gca tca gcc aat gag cca aaa att gat ttt aac cct ccc aat tat gta 152
Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn Tyr Val
      20                      25                      30

gaa gaa acc ccc tct aaa gaa ttt atc cct gaa ttg aac aag tta ggg 200
Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys Leu Gly
      35                      40                      45                      50

agt ttg ttt ggg cag ggt gag cgc ccc ttg ttt gcg gac agg agg gcg 248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala
      55                      60                      65

atg aag cct aac gat ttg atc aca atc att gtt tct gaa aaa gcg agc 296
Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys Ala Ser
      70                      75                      80

gcg aat tat tcc agc tct aaa gat tat aaa agc gct tca ggg ggt aat 344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn
      85                      90                      95

tcc acg ccc cca aga ctc act tat aac ggg cta gat gaa aga aag aaa 392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys
      100                      105                      110

aaa gaa gcg gag tat tta gac gat aag aat aat tac aat ttc acc aaa 440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys
      115                      120                      125                      130

tcc agc aat aac acg aat ttt aaa ggc ggt ggc tcg caa aaa aag agc 488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser
      135                      140                      145

gaa gat tta gag att gtg ttg agc gct cga atc att aag gtg cta gaa 536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu
      150                      155                      160

aac ggg aat tat ttc atc tat ggg aat aag gaa gtg cta gtg gat ggg 584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val Asp Gly
      165                      170                      175

gaa aag caa atc ctt aag gtg agt ggg gtg atc cgc cct tat gat att 632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile
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180	185	190	
gaa agg aat aac acc atc caa tcc aag ttt tta gcc gac gct aag att			680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile			
195	200	205	210
gaa tac acg aat tta ggg cat ttg agc gat tcc aat aag aag aaa ttc			728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe			
	215	220	225
gct gct gat gcg atg gaa acc caa atg cct tat taaaaagagc aaagcctagc			781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr			
	230	235	
atgagagcgga tcgctattgt tttagccaga agt			814
<210> 262			
<211> 237			
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<213> Helicobacter pylori			
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Tyr Val Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys			
	35	40	45
Leu Gly Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg			
	50	55	60
Arg Ala Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys			
	65	70	75
Ala Ser Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly			
	85	90	95
Gly Asn Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg			
	100	105	110
Lys Lys Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe			
	115	120	125
Thr Lys Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys			
	130	135	140
Lys Ser Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val			
	145	150	155
Leu Glu Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val			
	165	170	175
Asp Gly Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr			
	180	185	190
Asp Ile Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala			
	195	200	205
Lys Ile Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys			
	210	215	220
Lys Phe Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr			
	225	230	235

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Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser Gly Ala																
	5 10 15															
ttt tat acg gct cta gct gat gga atg cct gca aaa cag cag cac aat	152															
Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln His Asn																
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Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile Lys Gly																
	35 40 45 50															
aag caa gag cct aaa aac agc cat tta gtc gtt ttg atc gaa cct aaa	248															
Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu Pro Lys																
	55 60 65															
ata gag atc aat aaa gtt atc cct gaa agt tat caa aaa gag ttt gag	296															
Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu Phe Glu																
	70 75 80															
aag tct ttg ttt ctc cag ttg agt agt ttt tta gag aga aaa ggc tat	344															
Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys Gly Tyr																
	85 90 95															
agc gtt tcg caa ttt aaa gat gct agc gaa atc cct caa gac atc aaa	392															
Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp Ile Lys																
	100 105 110															
gaa aaa gcg ttg ctc gtt tta cgc atg gat ggg aat gtg gct atc ttg	440															
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	115 120 125 130															
gaa gat att gta gaa gag agc gat gcg ctt agc gaa gaa aaa gtg ata	488															
Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys Val Ile																
	135 140 145															
gac atg tct tca ggg tat ttg aac ttg aat ttt gtt gag cca aaa agt	536															
Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser																
	150 155 160															
gaa gat att atc cat agt ttt ggt att gat gtt tca aag att aag gct	584															
Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile Lys Ala																

165	170	175	
gtg att gaa aga gtg gaa ttg cgg cgc acc aat tct gga ggt ttt gtc			632
Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val			
180	185	190	
ccc aaa act ttt gtg cat agg att aag gaa acc gat cat gat caa gcc			680
Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Gln Ala			
195	200	205	210
att aga aaa atc atg aat caa gcc tat cac aaa gtg atg gtg cat att			728
Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val His Ile			
	215	220	225
acc aaa gag tta agc aaa aaa cac atg gaa cat tat gaa aaa gtt tct			776
Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser			
	230	235	240
agt gaa atg aaa aaa cga aag tagtttttaa gaaacgaaaa gcttaaaaat			827
Ser Glu Met Lys Lys Arg Lys			
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His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile			
35 40 45			
Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu			
50 55 60			
Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu			
65 70 75 80			
Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys			
85 90 95			
Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp			
100 105 110			
Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala			
115 120 125			
Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys			
130 135 140			
Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro			
145 150 155 160			
Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile			
165 170 175			
Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly			
180 185 190			
Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp			

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 Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Glu
 135 140 145

aat tta aaa ctc act ccc agt ctt aaa tct aaa atc gtt tat ggc gct 536
 Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr Gly Ala
 150 155 160

tct att tct caa gcc cat caa ttt gtc gct act aaa aac gct caa ata 584
 Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala Gln Ile
 165 170 175

ggc ttt gga gcg tta tcc ttg atg gat aaa aaa gat aaa aac ctc tct 632
 Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn Leu Ser
 180 185 190

tat ttc atc att gat aaa gcc ctt tat aac cct att gaa caa gcc ttg 680
 Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln Ala Leu
 195 200 205 210

att atc act aaa aat ggg gct aac aac cct tta gcc aaa gtc ttt aaa 728
 Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys
 215 220 225

gat ttt tta ttc agc cct aaa gcc aga gct att ttt aaa gaa tac ggc 776
 Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly
 230 235 240

tat att gtg gat taaaacgcat aaaaaaggcg agcaatggat catgagtttt 828
 Tyr Ile Val Asp
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tgattaccat gcg 841

<210> 266
 <211> 246
 <212> PRT
 <213> *Helicobacter pylori*

<400> 266
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 Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro
 35 40 45
 Lys Asp Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala
 50 55 60
 Gln Ile Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met
 65 70 75 80
 Ile Arg Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu
 85 90 95
 Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys
 100 105 110
 Met Asp Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala

85	90	95	
gtc gct aga aag ggt gat tta gtc tat ttt agg caa ttc aac aac caa			392
Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn Asn Gln			
100	105	110	
gcg ttt tta atc gct cct aat gat gaa ctc tat gag caa atc aga gcg			440
Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile Arg Ala			
115	120	125	130
act aac acc gat att aat ttt att agt tct gat ttg ttg gtt act ttt			488
Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val Thr Phe			
	135	140	145
ttg aat ggg ttt gac cca aaa atc gct aat tta agg aaa gcg tgc aac			536
Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala Cys Asn			
	150	155	160
gtt tat agc gtg ggg gtg att tat att gta acc acc aac acg ctc aat			584
Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr Leu Asn			
	165	170	175
att tta agt tgt gag agt ttt gaa att tta gaa aaa aga gag ctg gat			632
Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu Leu Asp			
	180	185	190
aca agc ggc gtt act aaa act tcc acg ccg ttt ttt tct agg gtt gag			680
Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg Val Glu			
195	200	205	210
ggg att gat gca ggc acg cta ggg aaa ctt ttt tca ggc agt cag tct			728
Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser Gln Ser			
	215	220	225
aaa aat tac ttc gct tac tat gac gct tta gtg aag aaa gaa aaa cgc			776
Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu Lys Arg			
	230	235	240
aaa gaa gtg agg att aaa aag agg gaa gaa aag att gat tct aga gaa			824
Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser Arg Glu			
	245	250	255
att aaa cga gaa atc aag caa gag gcc att aaa gag cct aaa aaa gcc			872
Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys Lys Ala			
	260	265	270
aat caa ggc aca caa aac gct cct act tta gaa gag aaa aac tac caa			920
Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn Tyr Gln			
275	280	285	290
aaa gca gag cgc aaa ctt gat gct aaa gaa gaa agg cgt tat ttg aga			968
Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr Leu Arg			
	295	300	305
gat gaa agg aaa aaa gcc aaa gcc acc aaa aag gct atg gaa ttt gaa			1016

Asp	Glu	Arg	Lys	Lys	Ala	Lys	Ala	Thr	Lys	Lys	Ala	Met	Glu	Phe	Glu		
			310					315					320				
gaa	aga	gaa	aaa	gag	cat	gat	gaa	agg	gac	gaa	caa	gag	act	gaa	gga	1064	
Glu	Arg	Glu	Lys	Glu	His	Asp	Glu	Arg	Asp	Glu	Gln	Glu	Thr	Glu	Gly		
			325				330					335					
aga	aga	aaa	gct	tta	gaa	atg	gat	aaa	ggc	gat	aaa	aaa	gaa	gaa	aga	1112	
Arg	Arg	Lys	Ala	Leu	Glu	Met	Asp	Lys	Gly	Asp	Lys	Lys	Glu	Glu	Arg		
			340				345					350					
gtc	aaa	ccc	aaa	gaa	aat	gag	cga	gaa	atc	aag	caa	gaa	gcc	att	aaa	1160	
Val	Lys	Pro	Lys	Glu	Asn	Glu	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys		
					360					365					370		
gag	cca	agt	gat	gga	aat	aac	gcc	acc	caa	caa	ggc	gaa	aaa	caa	aac	1208	
Glu	Pro	Ser	Asp	Gly	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Lys	Gln	Asn		
				375					380						385		
gct	cct	aaa	gag	aac	aac	gct	caa	aaa	gaa	gag	aat	aaa	cca	aat	tct	1256	
Ala	Pro	Lys	Glu	Asn	Asn	Ala	Gln	Lys	Glu	Glu	Asn	Lys	Pro	Asn	Ser		
			390					395						400			
aaa	gaa	gaa	aaa	cgc	cgc	ttg	aaa	gaa	gaa	aag	aaa	aaa	gcc	aaa	gcc	1304	
Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	Lys	Ala		
			405				410					415					
gaa	caa	aga	gcg	aga	gaa	ttt	gaa	caa	aga	gcg	aga	gag	cat	caa	gaa	1352	
Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His	Gln	Glu		
			420				425				430						
aga	gat	gaa	aaa	gag	ctt	gaa	gag	cga	aga	aag	gcg	cta	gaa	gcg	ggt	1400	
Arg	Asp	Glu	Lys	Glu	Leu	Glu	Arg	Arg	Lys	Ala	Leu	Glu	Ala	Gly			
					440				445					450			
aaa	aaa	taacatgtta	gaccaacaac	acatccaata	ctttaaaaac	ctagtagggg	1456										
Lys	Lys																

gag	1459
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<211> 452

<212> PRT

<213> Helicobacter pylori

<400> 268

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			20					25					30				
Asp	Leu	Pro	Lys	Lys	Ile	Ile	Arg	Phe	Pro	Ala	His	Asp	Leu	Gln	Val		
		35					40					45					
Gly	Glu	Phe	Gly	Phe	Val	Val	Thr	Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Val		
	50					55					60						

Asn	Ser	Glu	Val	Val	Ile	Ile	Ala	Val	Glu	Asn	Gly	Val	Ala	Thr	Ala	
65					70					75					80	
Lys	Phe	Arg	Ala	Phe	Glu	Ser	Met	Lys	Gln	Arg	His	Leu	Pro	Thr	Pro	
				85					90						95	
Arg	Met	Val	Ala	Arg	Lys	Gly	Asp	Leu	Val	Tyr	Phe	Arg	Gln	Phe	Asn	
			100					105					110			
Asn	Gln	Ala	Phe	Leu	Ile	Ala	Pro	Asn	Asp	Glu	Leu	Tyr	Glu	Gln	Ile	
		115					120						125			
Arg	Ala	Thr	Asn	Thr	Asp	Ile	Asn	Phe	Ile	Ser	Ser	Asp	Leu	Leu	Val	
	130					135					140					
Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu	Arg	Lys	Ala	
145					150					155					160	
Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr	Thr	Asn	Thr	
			165						170					175		
Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu	Lys	Arg	Glu	
		180						185					190			
Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe	Phe	Ser	Arg	
		195					200					205				
Val	Glu	Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	Ser	Gly	Ser	
	210					215					220					
Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val	Lys	Lys	Glu	
225					230					235					240	
Lys	Arg	Lys	Glu	Val	Arg	Ile	Lys	Lys	Arg	Glu	Glu	Lys	Ile	Asp	Ser	
			245						250					255		
Arg	Glu	Ile	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys	Glu	Pro	Lys	
		260						265					270			
Lys	Ala	Asn	Gln	Gly	Thr	Gln	Asn	Ala	Pro	Thr	Leu	Glu	Glu	Lys	Asn	
	275						280					285				
Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Leu	Asp	Ala	Lys	Glu	Glu	Arg	Arg	Tyr	
	290					295				300						
Leu	Arg	Asp	Glu	Arg	Lys	Lys	Ala	Lys	Ala	Thr	Lys	Lys	Ala	Met	Glu	
305					310					315					320	
Phe	Glu	Glu	Arg	Glu	Lys	Glu	His	Asp	Glu	Arg	Asp	Glu	Gln	Glu	Thr	
			325						330					335		
Glu	Gly	Arg	Arg	Lys	Ala	Leu	Glu	Met	Asp	Lys	Gly	Asp	Lys	Lys	Glu	
		340						345					350			
Glu	Arg	Val	Lys	Pro	Lys	Glu	Asn	Glu	Arg	Glu	Ile	Lys	Gln	Glu	Ala	
	355						360					365				
Ile	Lys	Glu	Pro	Ser	Asp	Gly	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Lys	
	370					375					380					
Gln	Asn	Ala	Pro	Lys	Glu	Asn	Asn	Ala	Gln	Lys	Glu	Glu	Asn	Lys	Pro	
385					390					395					400	
Asn	Ser	Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	
			405						410					415		
Lys	Ala	Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His	
		420						425					430			
Gln	Glu	Arg	Asp	Glu	Lys	Glu	Leu	Glu	Glu	Arg	Arg	Lys	Ala	Leu	Glu	
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Ala	Gly	Lys	Lys													
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 <212> DNA

<213> Helicobacter pylori

<220>

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<222> (74)...(943)

<400> 269

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          Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser
              1             5             10

agt tgg gta ggg acg att gtt att gtg ctg ttg gtt atc ttt ttt atc 157
Ser Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile
          15             20             25

gcg caa gcc ttt atc att ccc tct cgc tct atg gtt ggc acg ctc tat 205
Ala Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr
          30             35             40

gag ggc gac atg ctc ttt gtc aaa aag ttt tct tac ggc ata ccc att 253
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile
          45             50             55             60

cct aaa atc cca tgg att gag ctt cct gtt atg cct gat ttt aaa aat 301
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn
          65             70             75

aac gga cat ttg ata gag ggg gat cgc cct aag cgt ggc gaa gtg gtg 349
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val
          80             85             90

gtg ttt atc cct ccc cat gaa aaa aag tct tac tat gtt aaa agg aat 397
Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn
          95             100             105

ttt gcc att gga ggc gat gag gtg ttg ttc act aat gag ggt ttt tat 445
Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr
          110             115             120

ttg cac cct ttt gag agc gac acg gac aaa aat tac atc gct aaa cat 493
Leu His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His
          125             130             135             140

tac cct aac gcc atg aca aaa gaa ttt atg ggt aaa att ttt gtt tta 541
Tyr Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu
          145             150             155

aac cct tat aaa aat gag cat ccg ggt atc cat tac caa aaa gac aat 589
Asn Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn
          160             165             170

gaa acc ttc cac tta atg gag caa tta gcc act caa ggc gca gaa gct 637
Glu Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala
          175             180             185
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aat atc agc atg caa ctc att caa atg gag ggc gaa aag gtg ttt tat 685
Asn Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr
190 195 200

aag aaa atc aat gac gat gaa ttt ttc atg atc ggc gac aac aga gac 733
Lys Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp
205 210 215 220

aat tct agc gac tcg cgc ttt tgg ggg agt gtg gct tat aaa aac atc 781
Asn Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile
225 230 235

gtg ggt tcg cca tgg ttt gtt tat ttc agt ttg agt tta aaa aat agc 829
Val Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser
240 245 250

cta gaa atg gat gca gaa aat aac cct aaa aaa cgc tat ctg gtg cgt 877
Leu Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg
255 260 265

tgg gaa cgc atg ttt aaa agc gtt gga ggc tta gaa aaa atc att aaa 925
Trp Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys
270 275 280

aaa gaa aac gca acg cat taagggttttt tgtgcaatttt tttgatttct 973
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<212> PRT
<213> Helicobacter pylori

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Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met
35 40 45
Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro
50 55 60
Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu
65 70 75 80
Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro
85 90 95
Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly
100 105 110
Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe
115 120 125
Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala
130 135 140

Met	Thr	Lys	Glu	Phe	Met	Gly	Lys	Ile	Phe	Val	Leu	Asn	Pro	Tyr	Lys	
145					150					155					160	
Asn	Glu	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn	Glu	Thr	Phe	His	
				165					170						175	
Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala	Asn	Ile	Ser	Met	
			180					185					190			
Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr	Lys	Lys	Ile	Asn	
		195					200					205				
Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ser	Asp	
	210					215					220					
Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile	Val	Gly	Ser	Pro	
225					230					235					240	
Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp	
				245					250					255		
Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met	
		260					265						270			
Phe	Lys	Ser	Val	Gly	Gly	Leu	Glu	Lys	Ile	Ile	Lys	Lys	Glu	Asn	Ala	
	275						280					285				
Thr	His															
	290															

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 <213> Helicobacter pylori

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 tacagtgggt aaacgaaacg ggcgcattga gcctttggac attaccaaaa tccaaaaata 120
 cactaaggac gctacggaca atttagaggg cgtgagccaa agtgagctgg aagtggatgc 180
 gaggttgcaa ttcagggaca agatcactac tgaagaaatc caacaaactt tgattaaaac 240
 cgctgtggat aagatagata ttgacacgcc taattggagt tttgtcgcct caaggctttt 300
 tttgtatgat ttataccata aagtaagtgg ttttacaggg tataggcatt tgaaagagta 360
 ttttgaaaac gctgaagaaa agggccgcgc ccttaagggc tttaaggaaa aatttgatct 420
 agagttttta aatagccaga tcaagcctga aagggatttc caattcaatt atttagggat 480
 taaaaccttg tatgatcgct atttggttaa agacgctaac aacaacccta ttgaattgcc 540
 ccaacac atg ttt atg agc att gcg atg ttt tta gca caa aac gaa caa 589
 Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln
 1 5 10
 gaa ccc aat aaa atc gcc tta gaa ttt tat gaa gtt ttg agc aag ttt 637
 Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe
 15 20 25 30
 gaa gcg atg tgc gcg acc ccc act cta gcg aac gcc cgc acc acc aaa 685
 Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys
 35 40 45
 cac cag ctc agc tca tgc tat att ggc agc acg ccg gat aat att gag 733
 His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu

50	55	60	
ggg att ttt gac agc tat aag gaa atg gcg ctg ttg tcc aaa tac ggc Gly Ile Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly 65 70 75			781
gga ggg att ggc tgg gat ttt tct ttg gtg cgc tct att ggg agt tat Gly Gly Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr 80 85 90			829
att gat ggg cat aaa aat gcg agc gct ggc acg atc cct ttt tta aaa Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys 95 100 105 110			877
atc gct aac gat gtg gcg att gcg gtg gat caa tta ggc aca cga aag Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys 115 120 125			925
ggc gcg att gcg gtg tat ttg gaa att tgg cac att gat gtg atg gag Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu 130 135 140			973
ttc att gat tta agg aaa aat agc ggc gat gaa agg cga aga gcg cat Phe Ile Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His 145 150 155			1021
gat tta ttc ccg gct ctt tgg gtg tgc gat ttg ttt ttg aaa agg gtt Asp Leu Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val 160 165 170			1069
tta gaa gat gcg atg tgg act tta ttt gac cct tat gag tgt aag gat Leu Glu Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp 175 180 185 190			1117
ttg act gag ctt tat ggg cag gat ttt gaa aaa cgc tat tta gag tat Leu Thr Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr 195 200 205			1165
gaa aaa gat ccc aag atc att aag gaa tac att aac gct aaa gat tta Glu Lys Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu 210 215 220			1213
tgg aaa aaa atc tta atg aat tat ttt gaa gcc ggt ttg cct ttc tta Trp Lys Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu 225 230 235			1261
gcc ttt aaa gat aac gcc aat cgg tgc aac cca aac gct cat gca gga Ala Phe Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly 240 245 250			1309
atc att cga tcc agc aat cta tgc acg gag att ttc caa aat acc gcg Ile Ile Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala 255 260 265 270			1357
cct aac cac tac tac atg caa ata gaa tac acc gac ggc acc ata gag			1405

Pro	Asn	His	Tyr	Tyr	Met	Gln	Ile	Glu	Tyr	Thr	Asp	Gly	Thr	Ile	Glu		
				275					280					285			
ttt	ttt	gaa	gaa	aaa	gag	ttg	gta	acg	aca	gat	agt	aat	atc	act	aaa	1453	
Phe	Phe	Glu	Glu	Lys	Glu	Leu	Val	Thr	Thr	Asp	Ser	Asn	Ile	Thr	Lys		
		290						295					300				
tgc	gct	aac	aag	ctc	act	agc	acc	gat	att	cta	aag	ggc	aag	cca	atc	1501	
Cys	Ala	Asn	Lys	Leu	Thr	Ser	Thr	Asp	Ile	Leu	Lys	Gly	Lys	Pro	Ile		
		305						310				315					
tat	atc	gct	act	aaa	gtc	gct	aaa	gac	ggg	caa	acg	gcg	gtg	tgc	aat	1549	
Tyr	Ile	Ala	Thr	Lys	Val	Ala	Lys	Asp	Gly	Gln	Thr	Ala	Val	Cys	Asn		
	320						325				330						
ctg	gcg	agc	atc	aat	tta	agc	aaa	atc	aac	act	gaa	gaa	gac	att	aaa	1597	
Leu	Ala	Ser	Ile	Asn	Leu	Ser	Lys	Ile	Asn	Thr	Glu	Glu	Asp	Ile	Lys		
335					340					345					350		
agg	gtt	gtg	ccg	atc	atg	gtc	agg	ctt	tta	gac	aat	gtg	att	gat	ttg	1645	
Arg	Val	Val	Pro	Ile	Met	Val	Arg	Leu	Leu	Asp	Asn	Val	Ile	Asp	Leu		
				355					360					365			
aat	ttc	tac	cct	aac	cgc	aaa	gtc	aaa	gcc	act	aat	tta	caa	aat	agg	1693	
Asn	Phe	Tyr	Pro	Asn	Arg	Lys	Val	Lys	Ala	Thr	Asn	Leu	Gln	Asn	Arg		
			370					375					380				
gcc	ata	ggg	tta	ggg	gtt	atg	ggt	gaa	gcg	caa	atg	ctc	gca	gaa	cac	1741	
Ala	Ile	Gly	Leu	Gly	Val	Met	Gly	Glu	Ala	Gln	Met	Leu	Ala	Glu	His		
		385					390					395					
caa	atc	gct	tgg	ggg	tct	aaa	gag	cat	tta	gaa	aaa	att	gac	gct	tta	1789	
Gln	Ile	Ala	Trp	Gly	Ser	Lys	Glu	His	Leu	Glu	Lys	Ile	Asp	Ala	Leu		
	400					405					410						
atg	gag	caa	atc	agc	tac	cat	gcg	att	gac	acg	agc	gcg	aat	tta	gcg	1837	
Met	Glu	Gln	Ile	Ser	Tyr	His	Ala	Ile	Asp	Thr	Ser	Ala	Asn	Leu	Ala		
415					420					425				430			
aaa	gaa	aaa	ggg	gtt	tat	aag	gat	ttt	gaa	aat	tca	gaa	tgg	agt	aag	1885	
Lys	Glu	Lys	Gly	Val	Tyr	Lys	Asp	Phe	Glu	Asn	Ser	Glu	Trp	Ser	Lys		
			435					440					445				
ggg	att	ttc	ccc	att	gat	aaa	gcc	aat	aat	gaa	gcc	tta	aag	ctc	acc	1933	
Gly	Ile	Phe	Pro	Ile	Asp	Lys	Ala	Asn	Asn	Glu	Ala	Leu	Lys	Leu	Thr		
			450					455					460				
gaa	aaa	ggg	ctt	ttt	aat	cac	gct	tgc	gat	tgg	caa	ggt	ttg	agg	gaa	1981	
Glu	Lys	Gly	Leu	Phe	Asn	His	Ala	Cys	Asp	Trp	Gln	Gly	Leu	Arg	Glu		
		465					470					475					
aaa	gtc	aaa	gcc	aat	ggc	atg	cgt	aat	ggc	tat	tta	atg	gcg	atc	gct	2029	
Lys	Val	Lys	Ala	Asn	Gly	Met	Arg	Asn	Gly	Tyr	Leu	Met	Ala	Ile	Ala		
	480					485					490						

ccc aca agc tcc att tct att tta gta ggc aca acc caa acg att gaa 2077
Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu
495 500 505 510

ccc att tat aag aaa aaa tgg ttt gaa gaa aat ttg agc ggg ctt att 2125
Pro Ile Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile
515 520 525

cct gtt gtg gtg cct aat ttg aat gta gaa acc tgg aat ttt tac aca 2173
Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr
530 535 540

tca gcc tat gat att gac gct aaa gat ttg att aaa gca gcg gcc gtg 2221
Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Val
545 550 555

cgc caa aag tgg att gat caa ggc caa agc ctt aat gtg ttt tta cgc 2269
Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg
560 565 570

ata gaa aac gcc agc ggt aaa acc ttg cat gac atc tac acg ctc gct 2317
Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala
575 580 585 590

tgg aaa tta gga ctc aaa tcc act tat tat ttg cgc agc gaa agc cct 2365
Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro
595 600 605

agc ata gat gaa aaa agc gtg ttg gat cga tcg gtg gag tgt ttt aat 2413
Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn
610 615 620

tgc caa taatataagc ttaaataagc taatctttgc taaaatgaga tttaaaatta 2469
Cys Gln

ttta 2473

<210> 272
<211> 624
<212> PRT
<213> Helicobacter pylori

<400> 272
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Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe Glu Ala
20 25 30
Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys His Gln
35 40 45
Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu Gly Ile
50 55 60
Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly Gly Gly
65 70 75 80
Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr Ile Asp

Val	Val	Pro	Asn	Leu	Asn	Val	Glu	Thr	Trp	Asn	Phe	Tyr	Thr	Ser	Ala	
530						535					540					
Tyr	Asp	Ile	Asp	Ala	Lys	Asp	Leu	Ile	Lys	Ala	Ala	Ala	Val	Arg	Gln	
545					550					555					560	
Lys	Trp	Ile	Asp	Gln	Gly	Gln	Ser	Leu	Asn	Val	Phe	Leu	Arg	Ile	Glu	
				565					570					575		
Asn	Ala	Ser	Gly	Lys	Thr	Leu	His	Asp	Ile	Tyr	Thr	Leu	Ala	Trp	Lys	
			580					585					590			
Leu	Gly	Leu	Lys	Ser	Thr	Tyr	Tyr	Leu	Arg	Ser	Glu	Ser	Pro	Ser	Ile	
		595					600					605				
Asp	Glu	Lys	Ser	Val	Leu	Asp	Arg	Ser	Val	Glu	Cys	Phe	Asn	Cys	Gln	
610						615					620					

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 <213> Helicobacter pylori

<220>
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 <222> (56)...(1390)

<400> 273

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Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile	
5 10 15	
ata ctg gcc gct ggt aaa ggc act cgc atg cgt tct agc ctg cct aaa	154
Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys	
20 25 30	
act tta cac acc att tgt ggg gag cct atg ttg ttt tac att tta gaa	202
Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu	
35 40 45	
acg gct ttt tca atc agc gat gat gtg cat ctt atc tta cac cac caa	250
Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln	
50 55 60 65	
caa gaa cgc att aaa gaa gcg gtg ttg gag cgt ttt aag ggc gtc att	298
Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val Ile	
70 75 80	
ttt cac act caa att gtg gaa aaa tat tca ggg aca ggt ggg gct atc	346
Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala Ile	
85 90 95	
atg caa aaa gat aaa acg cct att tct acg aaa cat gag cgg gtt ttg	394
Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val Leu	
100 105 110	

att ttg aat gcg gac atg cct tta atc act aaa gac gct ctc gcc ccc	442
Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala Pro	
115 120 125	
tta tta gaa agc aag aat aac gct ata ggc tta ctc cat tta gct gac	490
Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala Asp	
130 135 140 145	
cct aaa ggt tat ggg cgc gtt gtt tta gaa aac cat cag gtt aaa aag	538
Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys Lys	
150 155 160	
att gta gaa gaa aag gac gct aat gat gaa gaa aaa gaa att aaa agc	586
Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys Ser	
165 170 175	
gtg aat gct ggc gtg tat ggg ttt gaa agg gat ttt tta gaa aaa tac	634
Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys Tyr	
180 185 190	
tta ccc aag ctc cat gac caa aac gcc caa aaa gaa tac tac ctc acg	682
Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu Thr	
195 200 205	
gat tta atc gct cta ggg atc aat gaa aac gaa aca att gac gct att	730
Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala Ile	
210 215 220 225	
ttc tta aaa gaa gag tgt ttt tta ggg gtg aat agc caa aca gaa agg	778
Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu Arg	
230 235 240	
gcg aaa gct gaa gaa atc atg cta gaa aga ctg cgc aaa aac gcc atg	826
Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala Met	
245 250 255	
gac ttg ggg gta gtg atg caa ttg cct aat agc att tat tta gaa aaa	874
Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu Lys	
260 265 270	
ggc gtg agt ttt aag ggg gag tgc gtt tta gag caa ggg gtg cgt ttg	922
Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg Leu	
275 280 285	
att ggg aat tgt ttg ata gaa aac gcg cat att aag gct tat agc gtg	970
Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser Val	
290 295 300 305	
ata gaa gag agc cag att gtt aat agc agt gtg ggg ccg ttt gcc cat	1018
Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala His	
310 315 320	
gcg cgc cct aaa agc gtg att tgt aat agc cat gtg ggg aat ttt gta	1066
Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe Val	

325	330	335	
gag act aaa aac gct aaa ctt caa ggc act aaa gca ggg cat ttg agc	1114		
Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu Ser			
340	345	350	
tat tta ggg gat tgt gag ata ggg aaa aac aca aat gta ggg gct ggc	1162		
Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala Gly			
355	360	365	
gtg atc act tgc aat tac gat ggt aaa aag aaa cac caa aca atc atc	1210		
Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile Ile			
370	375	380	385
ggg gaa aat gtc ttt ata ggg agc gat agc cag cta gtc gcc ccc ata	1258		
Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro Ile			
390	395	400	
aat atc ggc tct aat gtc tta atc ggc agc ggc acc act atc act aaa	1306		
Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr Lys			
405	410	415	
gac att cct agc ggt tcg ttg agc ctt tca cgc gcc cct caa acc aac	1354		
Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr Asn			
420	425	430	
att gaa aac ggg tat ttt aag ttt ttt aag aaa cct taatttggtt	1400		
Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro			
435	440	445	
gaataatgaa aaatcctaaa atattaatca tttacttta	1440		
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Lys Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu			
35 40 45			
Glu Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His			
50 55 60			
Gln Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val			
65 70 75 80			
Ile Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala			
85 90 95			
Ile Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val			
100 105 110			
Leu Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala			
115 120 125			
Pro Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala			

130	135	140
Asp Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys		
145	150	155
Lys Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys		
	165	170
Ser Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys		
	180	185
Tyr Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu		
	195	200
Thr Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala		
	210	215
Ile Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu		
225	230	235
Arg Ala Lys Ala Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala		
	245	250
Met Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu		
	260	265
Lys Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg		
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Leu Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser		
	290	295
Val Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala		
305	310	315
His Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe		
	325	330
Val Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu		
	340	345
Ser Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala		
	355	360
Gly Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile		
	370	375
Ile Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro		
385	390	395
Ile Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr		
	405	410
Lys Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr		
	420	425
Asn Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro		
	435	440
		445

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 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (227)...(715)

<221> misc_feature
 <222> 57
 <223> n = A,T,C or G

<400> 275

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 agtggaaaac gatattgaag tgggtattgt gattgggtgga ggcaatatta ttaggggggt 180
 tagcgcggct caagggggga ttattaggcg caccagtggg gattat atg ggc atg 235
 Met Gly Met

1

tta gcc acc gtg att aat gcg gta gcg atg caa gaa gct tta gag cat 283
 Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His
 5 10 15

atc ggc tta gac aca agg gtg cag agc gcg att gaa atc aaa gag att 331
 Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile
 20 25 30 35

tgt gaa agt tac att tac aga aaa gcg atc agg cat tta gaa aag ggt 379
 Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly
 40 45 50

agg gtg gtg att ttt ggc gca ggc acg gga aac ccg ttt ttc act acg 427
 Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr
 55 60 65

gat acg gct gcc act tta aga gcg att gaa att gga tcg gat tta atc 475
 Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile
 70 75 80

att aaa gcg act aaa gtg gat ggc att tac gac aaa gat cct aac aag 523
 Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys
 85 90 95

ttt aaa gac gct aaa aaa tta gac act tta agc tat aac gat gcc ttg 571
 Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn Asp Ala Leu
 100 105 110 115

ata ggg gat att gaa gtg atg gac gat acc gct att tct tta gct aaa 619
 Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser Leu Ala Lys
 120 125 130

gac aat aag ctc ccc att gtg gtg tgt aac atg ttc aaa aaa ggg aat 667
 Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys Lys Gly Asn
 135 140 145

tta ttg caa gtg atc aag cac caa caa ggc gta ttt tct atg gta aaa 715
 Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys
 150 155 160

taagcccttt aacattggat agaactcaaa ataaaaggat cagtttgaaa aaagag 771

<210> 276

<211> 163

<212> PRT

<213> Helicobacter pylori

<400> 276

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Leu	Glu	His	Ile	Gly	Leu	Asp	Thr	Arg	Val	Gln	Ser	Ala	Ile	Glu	Ile
			20					25					30		
Lys	Glu	Ile	Cys	Glu	Ser	Tyr	Ile	Tyr	Arg	Lys	Ala	Ile	Arg	His	Leu
		35					40					45			
Glu	Lys	Gly	Arg	Val	Val	Ile	Phe	Gly	Ala	Gly	Thr	Gly	Asn	Pro	Phe
	50					55					60				
Phe	Thr	Thr	Asp	Thr	Ala	Ala	Thr	Leu	Arg	Ala	Ile	Glu	Ile	Gly	Ser
65					70					75					80
Asp	Leu	Ile	Ile	Lys	Ala	Thr	Lys	Val	Asp	Gly	Ile	Tyr	Asp	Lys	Asp
			85						90					95	
Pro	Asn	Lys	Phe	Lys	Asp	Ala	Lys	Lys	Leu	Asp	Thr	Leu	Ser	Tyr	Asn
			100						105				110		
Asp	Ala	Leu	Ile	Gly	Asp	Ile	Glu	Val	Met	Asp	Asp	Thr	Ala	Ile	Ser
		115					120					125			
Leu	Ala	Lys	Asp	Asn	Lys	Leu	Pro	Ile	Val	Val	Cys	Asn	Met	Phe	Lys
	130					135					140				
Lys	Gly	Asn	Leu	Leu	Gln	Val	Ile	Lys	His	Gln	Gln	Gly	Val	Phe	Ser
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Met	Val	Lys													

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Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val Ala	
	5 10 15
tat gct aaa aat cct tca acg ctt tct aaa gaa gaa gag gtt ttg cag	154
Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu Gln	
	20 25 30
cat ttg caa agt ttt agc gcg cat ttc aag cag gtt tta aaa aat gaa	202
His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn Glu	
	35 40 45
aaa cct tta gtt tat tac ggg gtt tta aag gct aaa gcc cct aat tgg	250
Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn Trp	
	50 55 60 65
gct tta tgg gtt tat gaa aag cct tta aaa aaa gaa att tac atg aac	298

Ala	Leu	Trp	Val	Tyr	Glu	Lys	Pro	Leu	Lys	Lys	Glu	Ile	Tyr	Met	Asn		
				70					75					80			
gat	aaa	gaa	gtg	gta	att	tat	gag	cct	aat	ttg	ttt	caa	gcg	acc	atc	346	
Asp	Lys	Glu	Val	Val	Ile	Tyr	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Thr	Ile		
			85					90				95					
acg	ccc	tta	aaa	gac	aag	acg	gat	ttt	ttc	acc	att	ctc	aag	cgt	tta	394	
Thr	Pro	Leu	Lys	Asp	Lys	Thr	Asp	Phe	Phe	Thr	Ile	Leu	Lys	Arg	Leu		
		100					105					110					
aaa	aag	caa	gat	gac	gga	tct	ttt	aaa	acg	act	atc	aac	aaa	acc	act	442	
Lys	Lys	Gln	Asp	Asp	Gly	Ser	Phe	Lys	Thr	Thr	Ile	Asn	Lys	Thr	Thr		
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tat	cgt	ttg	gtt	ttt	aaa	gac	ggc	aag	cct	ttt	tca	ttg	gaa	ttt	aaa	490	
Tyr	Arg	Leu	Val	Phe	Lys	Asp	Gly	Lys	Pro	Phe	Ser	Leu	Glu	Phe	Lys		
130					135				140						145		
gat	gga	atg	aac	aat	ctt	gta	acg	atc	act	ttt	tct	caa	gca	gaa	atc	538	
Asp	Gly	Met	Asn	Asn	Leu	Val	Thr	Ile	Thr	Phe	Ser	Gln	Ala	Glu	Ile		
				150					155					160			
aac	ccc	acc	att	gct	aat	gaa	atc	ttt	ggt	ttt	aag	cct	aaa	gat	gaa	586	
Asn	Pro	Thr	Ile	Ala	Asn	Glu	Ile	Phe	Val	Phe	Lys	Pro	Lys	Asp	Glu		
			165				170					175					
aac	att	gat	att	gtg	cgc	caa	tgatttttta	tgatttcattg	catcttggtta							637	
Asn	Ile	Asp	Ile	Val	Arg	Gln											
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			20					25					30				
Gln	His	Leu	Gln	Ser	Phe	Ser	Ala	His	Phe	Lys	Gln	Val	Leu	Lys	Asn		
	35					40					45						
Glu	Lys	Pro	Leu	Val	Tyr	Tyr	Gly	Val	Leu	Lys	Ala	Lys	Ala	Pro	Asn		
	50				55					60							
Trp	Ala	Leu	Trp	Val	Tyr	Glu	Lys	Pro	Leu	Lys	Glu	Ile	Tyr	Met			
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Asn	Asp	Lys	Glu	Val	Ile	Tyr	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Thr			
			85					90					95				
Ile	Thr	Pro	Leu	Lys	Asp	Lys	Thr	Asp	Phe	Phe	Thr	Ile	Leu	Lys	Arg		
		100					105					110					
Leu	Lys	Lys	Gln	Asp	Asp	Gly	Ser	Phe	Lys	Thr	Thr	Ile	Asn	Lys	Thr		
	115						120					125					

Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe
 130 135 140
 Lys Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu
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 Glu Asn Ile Asp Ile Val Arg Gln
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<220>
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 aacaaggcta tgaattttaa aaaatccaca aagaagaaga attaaaagac aattttaaaag 180
 agcagttaga aaagcttaat gatcattctt tcacgcctaa agaatgggac actctttatt 240
 ctcaattcat cgctaataaa aacgatgact ataaggctaa aacgaaaaag atccaagaag 300
 atccgatttt taatctcacg ctagagaacg ggaaaaccaa aaacattaaa atcattgata 360
 agaaaaatat ccatagaaac gccttgcaag tgatccacca atacagcaat aaaggggggga 420
 agtatcaaaa ccgctatgat gtgagtatcc ttgtgaatgg cttgccttta gtgcatgtgg 480
 aattgaaaaa aagaggcgtg gcgatcaggg aggcgttcaa ccagatcaag cgctataaaa 540
 gggatagttt tagcgctgaa gacgggcttt ttgattttgt gcagattttt gtcacagta 600
 acggcacgag ctctaaatac tattcaaaca ccacaagaat agcccagctg gaaaaaaacc 660
 ataaagccga tacttttgaa ttcacgaatt attgggcgga tagcaagaat cacaattattg 720
 aggattha atg gat ttt gct aag gcg ttt ttt gca aag cgc agc ctt ttg 770
 Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu
 1 5 10
 aac gtt tta acg tgc tat tgc gtt ttc aca agc gaa gag gtt tta ttg 818
 Asn Val Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu
 15 20 25 30
 gtg atg cgg cct tat caa atc gtg gcg gcc gaa agg att ttg gaa aag 866
 Val Met Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys
 35 40 45
 atc aaa acc gcg caa aat agt aaa acg aaa aat caa agc aaa ggc tat 914
 Ile Lys Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr
 50 55 60
 atc tgg cac acg aca ggg agc ggt aaa acc cta acg agc ttt aaa agc 962
 Ile Trp His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser
 65 70 75
 gca acg ttg gct aaa gaa tta gag agc gtt tca aaa gtc ttg ttc gtg 1010
 Ala Thr Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val
 80 85 90

gtg gac agg aag gat ttg gac tat caa acc atg aaa gaa tac gat aaa	1058
Val Asp Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys	
95 100 105 110	
ttc caa aaa gat tgc gct aat tcc aac aca agc act aag att tta aaa	1106
Phe Gln Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys	
115 120 125	
gaa cag ctt gaa gat tct aac gct aaa atc att atc acc acg atc caa	1154
Glu Gln Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln	
130 135 140	
aaa tta gac aaa ttc gtt aaa tcc cat aaa ggg cat gcg att ttt aat	1202
Lys Leu Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn	
145 150 155	
gaa gaa gtt gtg atg att ttt gat gaa tgc cac agg agt cag tta ggc	1250
Glu Glu Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly	
160 165 170	
tct atg cat caa gcc atc act aaa gcg ttt aaa aaa tac cac ctt ttt	1298
Ser Met His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe	
175 180 185 190	
ggc ttt act ggc acg ccc att ttt gca gct aat tgc gat aaa aac aac	1346
Gly Phe Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn	
195 200 205	
cct tta ggc acg aca gag caa aag ttt ggg aaa tgc ctc cac caa tac	1394
Pro Leu Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr	
210 215 220	
acc att att gat gcg atc agg gat aaa aac gtt ttg ccc ttt aga gtg	1442
Thr Ile Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val	
225 230 235	
gaa tac cac aac acc att aaa gct aaa gag gac att aag gat aat aag	1490
Glu Tyr His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys	
240 245 250	
gtt aga gcg gtt gat gaa aaa aac gcc ctt ttg gat act agg agg atc	1538
Val Arg Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile	
255 260 265 270	
aaa gaa atc act aaa tgc att tta gag cgt ttc aat caa gcc act aaa	1586
Lys Glu Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys	
275 280 285	
aat aaa aaa ttc aat tcc att ctg gca tgc tct agc ata gaa gcg ctg	1634
Asn Lys Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu	
290 295 300	
aaa aaa tac tac caa gcc ttt aaa gaa gaa aaa cac gat ctt aaa atc	1682
Lys Lys Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile	

305	310	315	
gct gcc att ttt agc tat Ala Ala Ile Phe Ser Tyr 320	agc gct aat gag gaa Ser Ala Asn Glu Glu 325	att gac acg cta gaa Ile Asp Thr Leu Glu 330	1730
gat gaa aac aat gaa agc Asp Glu Asn Asn Glu Ser 335	gct tgc cgg cta gac Ala Cys Arg Leu Asp 340	aaa agc tca agg gat Lys Ser Ser Arg Asp 345	1778
ttt tta gag ggc gcg att Phe Leu Glu Gly Ala Ile 355	gcg gat tat aat ggg Ala Asp Tyr Asn Gly 360	atg ttt ggc gtt tct Met Phe Gly Val Ser 365	1826
ttt gac act tcg gat caa Phe Asp Thr Ser Asp 370	aaa ttc caa agt tat Lys Phe Gln Ser Tyr 375	tac aag gat ctt tct Tyr Lys Asp Leu Ser 380	1874
caa aaa atg aaa gag cgt Gln Lys Met Lys Glu Arg 385	aaa atc gat ctt tta Lys Ile Asp Leu Leu 390	atg gtg gtg aac atg Met Val Val Asn Met 395	1922
ttt ttg acc ggg ttt gac Phe Leu Thr Gly Phe Asp 400	gct aca agg ctc aac Ala Thr Arg Leu Asn 405	acc ctt tgg gtg gat Thr Leu Trp Val Asp 410	1970
aaa aat ctc aaa tac cat Lys Asn Leu Lys Tyr His 415	ggg cta att caa gct Gly Leu Ile Gln Ala 420	ttt tca cgc gca aac Phe Ser Arg Ala Asn 425	2018
cgc att tta gat agc gtt Arg Ile Leu Asp Ser Val 435	aaa acg cat ggg aat Lys Thr His Gly Asn 440	atc gtg tgt ttt agg Ile Val Cys Phe Arg 445	2066
gat tta gaa cag gat ttg Asp Leu Glu Gln Asp Leu 450	aat gac gct ctc atg Asn Asp Ala Leu Met 455	ctt ttt ggc aac aag Leu Phe Gly Asn Lys 460	2114
gac gct caa tct att gcg Asp Ala Gln Ser Ile Ala 465	ctg tta aga aaa tat Leu Leu Arg Lys Tyr 470	gaa gat tat ttg aaa Glu Asp Tyr Leu Lys 475	2162
ggc tac acg gat aac aac Gly Tyr Thr Asp Asn Asn 480	aaa gaa tac gag ggc Lys Glu Tyr Glu Gly 485	tat gag ggt ttg att Tyr Glu Gly Leu Ile 490	2210
aaa agg ctt tta acc gaa Lys Arg Leu Leu Thr Glu 495	ttc cca tta aaa gag Phe Pro Leu Lys Glu 500	cca atc gtt tca gaa Pro Ile Val Ser Glu 505	2258
agc cag aaa aag gat ttt Ser Gln Lys Lys Asp Phe 515	att aag ctt ttt ggc Ile Lys Leu Phe Gly 520	aag att ttg aaa tta Lys Ile Leu Lys Leu 525	2306
gaa aat att tta aac agc gaa aat ttc aaa aaa 530	gac gat tac atc 535		2354

Glu Asn Ile Leu Asn Ser Phe Glu Asn Phe Lys Lys Asp Asp Tyr Ile	
530 535 540	
aat ccc agg gat ttt caa gac tat caa agc aaa tac ctt gat ttt tac	2402
Asn Pro Arg Asp Phe Gln Asp Tyr Gln Ser Lys Tyr Leu Asp Phe Tyr	
545 550 555	
gat gca atg aga tca gaa aaa ggg aag gat aaa gaa gag att aat gat	2450
Asp Ala Met Arg Ser Glu Lys Gly Lys Asp Lys Glu Glu Ile Asn Asp	
560 565 570	
gat ttg att ttt gaa att gaa ctc atc aaa caa gtg gaa gtc aat att	2498
Asp Leu Ile Phe Glu Ile Glu Leu Ile Lys Gln Val Glu Val Asn Ile	
575 580 585 590	
gac tat att ttg aat ttg att gaa gag ttc gct aaa gag cat ggg gtg	2546
Asp Tyr Ile Leu Asn Leu Ile Glu Glu Phe Ala Lys Glu His Gly Val	
595 600 605	
gaa atc caa ggc gtt aaa acc aaa ata gag cca atc atc aac tcc agc	2594
Glu Ile Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser	
610 615 620	
ata gag tta agg aat aaa aaa gat ttg atc atg gat ttc att gac aaa	2642
Ile Glu Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys	
625 630 635	
tac aac aaa gac caa gaa gtc cat gcg cat ttt caa gat tat atc cac	2690
Tyr Asn Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His	
640 645 650	
caa aaa aga gaa gag gaa ttc caa aat atc ata gaa gaa aac cgc ttg	2738
Gln Lys Arg Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu	
655 660 665 670	
aat gaa gaa aaa gcc tat tcg ttc atg cag cat gcc ttt aaa ggg ggc	2786
Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly	
675 680 685	
gaa atc agt ttt agt ggg acg gaa ttc cct aaa atc att gaa gaa aaa	2834
Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys	
690 695 700	
ccc tcc atg ttt ggt aaa aat tcg cgc tat caa gag gtg aaa gaa aaa	2882
Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys	
705 710 715	
gtc gct gca agc ctt tct cgt ttt ttc cac cgc ttt tgt gat ctc act	2930
Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr	
720 725 730	
agc gct ata ttt aag aaa aat gag gtt aaa aaa gat gag gtt aat gaa	2978
Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu	
735 740 745 750	

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Lys

gatt 3035

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35 40 45
Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr Ile Trp
50 55 60
His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser Ala Thr
65 70 75 80
Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val Val Asp
85 90 95
Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys Phe Gln
100 105 110
Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys Glu Gln
115 120 125
Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln Lys Leu
130 135 140
Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn Glu Glu
145 150 155 160
Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly Ser Met
165 170 175
His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe Gly Phe
180 185 190
Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn Pro Leu
195 200 205
Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr Thr Ile
210 215 220
Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val Glu Tyr
225 230 235 240
His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys Val Arg
245 250 255
Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile Lys Glu
260 265 270
Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys Asn Lys
275 280 285
Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu Lys Lys
290 295 300
Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile Ala Ala
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      Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile
        1             5             10

ggt ggt atg agt tta aac gct aaa gat ccg aat gtg ttg cgt aag att 157
Val Val Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile
  15             20             25             30

ggt ttt gag aaa tgt ctg cct aat tat gag aaa aat cag aat cct tcg 205
Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser
             35             40             45

cca tgc ata gaa gtc aaa ccc gat gcc ggc tat gtg gtt tta aaa gat 253
Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp
             50             55             60

att aac ggc ccg ttg caa tat ttg ttg atg cca aca act cac att agc 301
Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser
             65             70             75

ggt att gaa agc cct ttg tta ctt gat cct tct acg cct aac ttt ttt 349
Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe
  80             85             90

tat tta tcc tgg caa gcg cgt gat ttt atg agt aaa aaa tac ggc caa 397
Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln
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ccc att cct gat tat gcg att tct ttg acg att aac tct agc aaa ggg 445
Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly
             115             120             125

cga tcg caa aac cat ttt cat atc cat atc tct tgc att agt ctt gaa 493
Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu
             130             135             140

gca cgc aaa cag ctg gat aat aac cta aaa aaa atc aac agc cgt tgg 541
Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp
             145             150             155

tcg cca tta ccg ggc ggt ttg aat ggg cat aaa tac ttg gcg cgt cgg 589
Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg
  160             165             170

gta aca gag agc gag tta gtg caa aaa agc ccg ttt gtc atg ctt aat 637
Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn

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Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala				
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gtg gtg caa caa agc gat aac tcc ttt gtc tta tta gcg aca caa ttt				733
Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe				
	210	215	220	
aac cca ttg act tta aat cgc gct tca gcc gaa gag att caa gat cat				781
Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His				
	225	230	235	
gaa tgc gcg att ttg cac taaagcgagt tagattctta agcttgagcg				829
Glu Cys Ala Ile Leu His				
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Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys				
35 40 45				
Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn				
50 55 60				
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile				
65 70 75 80				
Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu				
85 90 95				
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile				
100 105 110				
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser				
115 120 125				
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg				
130 135 140				
Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro				
145 150 155 160				
Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr				
165 170 175				
Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu				
180 185 190				
Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val				
195 200 205				
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro				
210 215 220				
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys				

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Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met Pro	
150 155 160	
aag aga cag aag gct tta gag ggt aaa gaa aat tta cct aag cgt gag	587
Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg Glu	
165 170 175	
agt ttg ccc tgg ttt gca acc att tca aaa gag agc atg ttt gtg tcc	635
Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val Ser	
180 185 190	
tta tgc cat gcg tgc ggg att aaa agc gct gaa gtg caa ggc ttg aaa	683
Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu Lys	
195 200 205	
ctg ggt caa aac agc gtg gtg aaa aac gct cct aga gtg gaa gtg tat	731
Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val Tyr	
210 215 220 225	
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Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys Glu	
230 235 240	
gtt ttt atc ccg ttg aat cgt cat aaa gac atg cag tta gat tct gcc	827
Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser Ala	
245 250 255	
tta ttg gcg act ttt ggc gat gct ttt gcc ctt gtg gat ggt agg gat	875
Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg Asp	
260 265 270	
tta ggc aat tac gag agc aaa ctt ttt gaa aaa aga gtg tcc tat acg	923
Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr Thr	
275 280 285	
att gtc taaaggcatg aaatctagga atattccttg atagcgggct ttccttttta	979
Ile Val	
290	
gg	981
<210> 284	
<211> 291	
<212> PRT	
<213> Helicobacter pylori	
<400> 284	
Met Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly	
1 5 10 15	
Ala Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser	
20 25 30	
Val Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser	
35 40 45	
Ala Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser	

gct tgg gtt ttt gaa gac gct aaa gcc ccc tac gaa gaa atg ggc gtg 255
Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val
45 50 55

gcg tat atc cct gtt aat aat aaa tat tta ggg att gag caa gcg acc 303
Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr
60 65 70

tta aac gct aaa ttg agt ctg atc gtg gtt ttt cat gaa atc atg atg 351
Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met
75 80 85 90

aag tat aaa aaa cgc ttc atg gag caa ttc cat gag tcc gag cag acg 399
Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr
95 100 105

act acg aat atc agt tac gct atc tat aat tat cta gcg act aag atc 447
Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile
110 115 120

cag gta tcc aac acc tac acg aat tta aaa tcg gag gtg gcg gtg gtg 495
Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val
125 130 135

aaa atc aag cta gtg ggt tgt cag att gag caa atc aaa agg tat tta 543
Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu
140 145 150

aaa gcg agc gtt gaa aac ctt aac gat aat gaa atc gct tac atc gct 591
Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala
155 160 165 170

aag gtc gct caa aaa gaa ttt ggt agc gtt tgt gcg tta agg 633
Lys Val Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg
175 180

tagttttata gcattctagc gagcatgttt aaggcatgct ctacgctttt att 686

<210> 286

<211> 184

<212> PRT

<213> Helicobacter pylori

<400> 286

Met Val Leu Ile Ala Leu Leu Gly Val Phe Ser Ser Val Ser Leu Ser
1 5 10 15
Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val Ser Asp Leu Lys
20 25 30
Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Glu Asp
35 40 45
Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn
50 55 60
Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser
65 70 75 80

Leu	Ile	Val	Val	Phe	His	Glu	Ile	Met	Met	Lys	Tyr	Lys	Lys	Arg	Phe		
				85					90					95			
Met	Glu	Gln	Phe	His	Glu	Ser	Glu	Gln	Thr	Thr	Thr	Asn	Ile	Ser	Tyr		
			100					105					110				
Ala	Ile	Tyr	Asn	Tyr	Leu	Ala	Thr	Lys	Ile	Gln	Val	Ser	Asn	Thr	Tyr		
		115					120					125					
Thr	Asn	Leu	Lys	Ser	Glu	Val	Ala	Val	Val	Lys	Ile	Lys	Leu	Val	Gly		
	130					135					140						
Cys	Gln	Ile	Glu	Gln	Ile	Lys	Arg	Tyr	Leu	Lys	Ala	Ser	Val	Glu	Asn		
145					150					155					160		
Leu	Asn	Asp	Asn	Glu	Ile	Ala	Tyr	Ile	Ala	Lys	Val	Ala	Gln	Lys	Glu		
			165						170					175			
Phe	Gly	Ser	Val	Cys	Ala	Leu	Arg										
			180														

<210> 287
 <211> 310
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (112)...(252)

<400> 287
 atgcctgccca tttcatagcc taaatcttct ttagagccga attgataagc ggctttttaag 60
 acttcttttt gcttagcggtt aaaatcttta atattgtcgc aattgggtcat c atg act 117
 Met Thr
 1

tta gta acg ggc gat ttg ggc ttg ttt tta acc cct tta gcg ggc tta 165
 Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala Gly Leu
 5 10 15

ggc tct gtt tta gtg ggg ctt tct gtt gcg gct aaa ctt aaa gat gca 213
 Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys Asp Ala
 20 25 30

ctt aag gct gtg cct agc cat aag gct tta aag atg gtg tgagtgagtg 262
 Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
 35 40 45

gggttaaagc tttcaaaacg cctacctttt gtattaagaa ataaacta 310

<210> 288
 <211> 47
 <212> PRT
 <213> Helicobacter pylori

<400> 288
 Met Thr Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala
 1 5 10 15
 Gly Leu Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys
 20 25 30

Asp Ala Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
 35 40 45

<210> 289
 <211> 631
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (145)...(579)

<221> misc_feature
 <222> 48
 <223> n = A,T,C or G

<400> 289
 gcgttcaata gaatgcttta gtttaggaagc tccttgcttt agcaaggngt ggtttccactg 60
 aaagagagta agaaatttga agaaagggtt tatctttttt tagatgaatt tgtgcgctttt 120
 ggtaaatgac cttttttatt agaa atg cca gca tta agt agg agc tat ggt 171
 Met Pro Ala Leu Ser Arg Ser Tyr Gly
 1 5

gtg gtt tta att ttt atc acg caa tcc aac gct ctt att gaa aaa tat 219
 Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr
 10 15 20 25

tac ggc aga gaa gat gca aga att gtt aat agc acc gtg gct tac aaa 267
 Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys
 30 35 40

ata att ttc aaa atg gat gat tta gaa tac gct aaa cag gtg agc gaa 315
 Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu
 45 50 55

gaa gtc ggt aag atg act aga aaa aca cga agc cac tct aca gaa aaa 363
 Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys
 60 65 70

gga caa ctc att acc gga ggg act tct agt ata ggt aaa gag gcg tgg 411
 Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp
 75 80 85

gac tta ttg agc gcg caa gat att atg aat att gat aaa gat gaa gtg 459
 Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val
 90 95 100 105

atc gtt tta gta agc ggt cat aag gct aaa ccc tta aaa tta aaa gcg 507
 Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala
 110 115 120

aat tat tat ttc aaa aac aaa gaa tta ctc tct cgt att aac tgg gaa 555
 Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Leu Ser Arg Ile Asn Trp Glu
 125 130 135

gtc aag ccc aat gaa gaa gtg ttt tgatggatta aaaaagtttg catgagtatt 609
 Val Lys Pro Asn Glu Glu Val Phe
 140 145

ttttaattgc ttttttaaaa at 631

<210> 290
 <211> 145
 <212> PRT
 <213> Helicobacter pylori

<400> 290
 Met Pro Ala Leu Ser Arg Ser Tyr Gly Val Val Leu Ile Phe Ile Thr
 1 5 10 15
 Gln Ser Asn Ala Leu Ile Glu Lys Tyr Tyr Gly Arg Glu Asp Ala Arg
 20 25 30
 Ile Val Asn Ser Thr Val Ala Tyr Lys Ile Ile Phe Lys Met Asp Asp
 35 40 45
 Leu Glu Tyr Ala Lys Gln Val Ser Glu Glu Val Gly Lys Met Thr Arg
 50 55 60
 Lys Thr Arg Ser His Ser Thr Glu Lys Gly Gln Leu Ile Thr Gly Gly
 65 70 75 80
 Thr Ser Ser Ile Gly Lys Glu Ala Trp Asp Leu Leu Ser Ala Gln Asp
 85 90 95
 Ile Met Asn Ile Asp Lys Asp Glu Val Ile Val Leu Val Ser Gly His
 100 105 110
 Lys Ala Lys Pro Leu Lys Leu Lys Ala Asn Tyr Tyr Phe Lys Asn Lys
 115 120 125
 Glu Leu Leu Ser Arg Ile Asn Trp Glu Val Lys Pro Asn Glu Glu Val
 130 135 140
 Phe
 145

<210> 291
 <211> 290
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (106)...(237)

<400> 291
 taagggctta cgcataaaat cgcacccgcg ccgatttttt gagcgaactt tgctaaagaa 60
 agggactcgc tcgtggcggtt actgcccacg ccggctaaca ctttc atg cgc gaa ttt 117
 Met Arg Glu Phe
 1

gag ggc gtt tta gtg ttt ttg caa gtt tct atg gcg att tca atg caa 165
 Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln
 5 10 15 20

cgc atg tgc tct ttg tgg gtg agc gtg gcg gat tct cct gtc gtg cca 213

Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro
25 30 35

aca ggc acg cat gcg tcc atg ccc tgaaaaattt ggcgcttgat caaggtttca 267
Thr Gly Thr His Ala Ser Met Pro
40

taagcggcct catcaacgct caa 290

<210> 292
<211> 44
<212> PRT
<213> Helicobacter pylori

<400> 292
Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala
1 5 10 15
Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser
20 25 30
Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro
35 40

<210> 293
<211> 421
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (58)...(369)

<400> 293
aaagaagggtt tgaaaagcctt ttttaaaagg cttttgaagt atttggggta ggcttga atg 60
Met
1

aaa gtg caa aat ttt atc cat ttt tct gtt gtg gta ggg ttt ttt ttg 108
Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe Leu
5 10 15

ggg tta gtg ttt tcg gtg ttg aaa ttc aat gag cca gag agc att tta 156
Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile Leu
20 25 30

tta tgg acg gtg tta tcc acg ctt ggg ggg tac ttg att gcg ttg ttg 204
Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu Leu
35 40 45

ttt gcg tct att ttt atc gct tgc acg gat ttg gat att tgt ctt ttt 252
Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu Phe
50 55 60 65

gac aaa aaa ggc act gaa gag agt ttg ctt cgt ttc aac cat gag ttt 300
Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu Phe

70	75	80	
aaa aac aga gaa aaa gaa gtg gct agt att tta gaa tac att aga agt			348
Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg Ser			
85	90	95	
tat gat ttt gat gat gga aaa tagaatgccc aaaggaattc aaaaaactga			399
Tyr Asp Phe Asp Asp Gly Lys			
100			
aacaagcgaa aaaaatatag aa			421
 <210> 294			
<211> 104			
<212> PRT			
<213> Helicobacter pylori			
 <400> 294			
Met Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe			
1	5	10	15
Leu Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile			
20	25	30	
Leu Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu			
35	40	45	
Leu Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu			
50	55	60	
Phe Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu			
65	70	75	80
Phe Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg			
85	90	95	
Ser Tyr Asp Phe Asp Asp Gly Lys			
100			
 <210> 295			
<211> 670			
<212> DNA			
<213> Helicobacter pylori			
 <220>			
<221> CDS			
<222> (51)...(617)			
 <400> 295			
gttttagaaaa gcgtttgaac gctataaaaa atgcagagtg gctttaaggc atg aaa			56
		Met Lys	
		1	
aag att gca ttt ttt att ttt gtc att ttg ttt tcg gta ggg att tat			104
Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr			
5	10	15	
tta att tgg cat gtt tta ttg gaa aaa gcc cta gaa ttg aaa tta gca			152
Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala			
20	25	30	

acc tca gct aat gat ttg ctt tta aaa ttg ttg gca att ctt ggc gtt 200
 Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val
 35 40 45 50
 ttt tca atg tta gtg ctt ttt caa ggc att att tct tcg tat aag aag 248
 Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys
 55 60 65
 cgc caa ctc aaa cgc att tta caa aaa ata gac gcc atg aac ggc ttt 296
 Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe
 70 75 80
 gaa ttt gaa gaa tat tcc aaa atc ttt ttc act tca aag ggt ttt gaa 344
 Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu
 85 90 95
 gtg agc atc acg caa aaa agc ggc gat tat gga gcg gat ttg att ata 392
 Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile
 100 105 110
 gaa aaa gac ggc atc aag tgg gcg gtt caa gtc aaa cgc tac tcg cat 440
 Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His
 115 120 125 130
 aaa gtt tcg ccc aaa gcc att caa gag gtg gtc tct tct aaa gct tat 488
 Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys Ala Tyr
 135 140 145
 tac gct tgc gaa aaa gct tgc gtg atc acc aac agc tat ttc acg caa 536
 Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe Thr Gln
 150 155 160
 gcc gct caa aaa ctg gct caa gct aac gaa gtg ctc ttg att gac aga 584
 Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile Asp Arg
 165 170 175
 gac gaa tgg gtc agg ttt ttg aac gaa aag aga tgaaccgatc ccatcagatc 637
 Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
 180 185

gtttggttctc aagttctttt aaaattttgt cgt 670

<210> 296

<211> 189

<212> PRT

<213> *Helicobacter pylori*

<400> 296

Met Lys Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly
 1 5 10 15
 Ile Tyr Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys
 20 25 30
 Leu Ala Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu
 35 40 45

Gly Val Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr
 50 55 60
 Lys Lys Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn
 65 70 75 80
 Gly Phe Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly
 85 90 95
 Phe Glu Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu
 100 105 110
 Ile Ile Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr
 115 120 125
 Ser His Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys
 130 135 140
 Ala Tyr Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe
 145 150 155 160
 Thr Gln Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile
 165 170 175
 Asp Arg Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
 180 185

<210> 297
 <211> 600
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (125)...(538)

<400> 297
 caaagagtgg gataaaatca cagaaatttg taagagagcg ctagctttta gataacaaaa 60
 agatcatggc attttgtatt tgcttaataa cactataata aaatttttaa taaggagata 120
 catc atg tta gaa aat gtc aaa aag tcc ttt ttt agg gtt ttg tgc ttg 169
 Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu
 1 5 10 15
 ggt gcg ttg tgt tta ggg ggg cta atg gca gag caa gac cct aaa gag 217
 Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu
 20 25 30
 ctt gtg ggt ttg ggg gca aag agc tac aaa gag aaa gat ttc act caa 265
 Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln
 35 40 45
 gcg aag aaa tat ttt gag aaa gcg tgc gat ttg aaa gaa aat agc ggg 313
 Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly
 50 55 60
 tgt ttt aat tta ggg gtg ctt tat tat caa ggg caa ggg gtg gaa aag 361
 Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys
 65 70 75
 aac ttg aaa aaa gcc gcc tcc ttt tac gct aaa gct tgc gat ttg aat 409
 Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn
 80 85 90 95

tac agc aat ggg tgt cat ttg cta ggg aat tta tat tac agc ggg caa 457
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln
100 105 110

ggc gtg tcc caa aac acc aat aaa gcc cta caa tac tac tct aaa gcg 505
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala
115 120 125

tgc gat ttg aaa tac gct gaa ggg tgc gcg act taggggggat ttatcatgat 558
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
130 135

ggtaaagtgg taactaggga ttttaaaaaa gcggtggaat at 600

<210> 298
<211> 138
<212> PRT
<213> Helicobacter pylori

<400> 298
Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly
1 5 10 15
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
20 25 30
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala
35 40 45
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
50 55 60
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn
65 70 75 80
Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr
85 90 95
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
100 105 110
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
115 120 125
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
130 135

<210> 299
<211> 879
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (59)...(826)

<400> 299
ttttaagatt ggtagccatt ggcattatgt ttgatcttat taaagcagag gagtaaca 58
atg gga tac gca agc aaa tta gcc ttg aag att tgt ttg gca agt tta 106
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
1 5 10 15

tgt tta ttt agc gct ctt ggt gca gaa cac ctt gaa caa aaa agg aac	154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn	
20 25 30	
tat att tat aam ggg gag gaa gcc tat aat aat aag gaa tat gag cgg	202
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg	
35 40 45	
gcg gct tct ttt tat aag agc gcg att aaa aat ggc gag ccg ctt gct	250
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala	
50 55 60	
tat gtt ctt tta ggg atc atg tat gaa aat ggt agg ggt gtg cct aaa	298
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys	
65 70 75 80	
gat gaa aag aaa gcg gct gaa tat ttt caa aaa gcg gtt gat aac gat	346
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp	
85 90 95	
ata cct aga ggg tat aac aat tta ggc gtg atg tat aaa gag ggt aga	394
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg	
100 105 110	
ggt gtg cct aaa gat gaa aag aaa gcc gtg gag tat ttt aga ata gct	442
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala	
115 120 125	
acc gag aag ggc tat act aac gcc tat ata aac tta ggc atc atg tat	490
Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr	
130 135 140	
atg gag ggt agg gga gtt cca agc aac tat gtg aaa gcg aca gag tgc	538
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys	
145 150 155 160	
ttt aga aaa gcg atg cat aag ggt aat gta gaa gct tat atc ctt tta	586
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu	
165 170 175	
ggg gat att tat tat agt ggg aat gat caa ttg ggt att gag cca gac	634
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp	
180 185 190	
aaa gat aag gcg att gtc tat tat aaa atg gcg gct gat atg agc tct	682
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser	
195 200 205	
tct aga gct tat gaa ggg tta gca gag tct tat cag tat ggg tta ggc	730
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly	
210 215 220	
gtg gaa aaa gat aag aaa aag gct gaa gaa tac atg caa aaa gca tgc	778
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys	

225	230	235	240	
gat ttt gac att gat aaa aat tgt aag aaa aag aac act tca agc cga 826				
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg				
	245	250	255	

taactctcaa acttgggctt gattaggatt ttgttttat ttttaagtagc atg 879

<210> 300
 <211> 256
 <212> PRT
 <213> Helicobacter pylori

<220>
 <221> VARIANT
 <222> 36
 <223> Xaa = Any Amino Acid

<400> 300

Met	Gly	Tyr	Ala	Ser	Lys	Leu	Ala	Leu	Lys	Ile	Cys	Leu	Ala	Ser	Leu
1				5				10						15	
Cys	Leu	Phe	Ser	Ala	Leu	Gly	Ala	Glu	His	Leu	Glu	Gln	Lys	Arg	Asn
			20					25					30		
Tyr	Ile	Tyr	Xaa	Gly	Glu	Glu	Ala	Tyr	Asn	Asn	Lys	Glu	Tyr	Glu	Arg
		35					40					45			
Ala	Ala	Ser	Phe	Tyr	Lys	Ser	Ala	Ile	Lys	Asn	Gly	Glu	Pro	Leu	Ala
	50					55					60				
Tyr	Val	Leu	Leu	Gly	Ile	Met	Tyr	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys
65					70					75				80	
Asp	Glu	Lys	Lys	Ala	Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp	
			85					90					95		
Ile	Pro	Arg	Gly	Tyr	Asn	Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Arg
			100					105					110		
Gly	Val	Pro	Lys	Asp	Glu	Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala
		115					120					125			
Thr	Glu	Lys	Gly	Tyr	Thr	Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr
	130					135					140				
Met	Glu	Gly	Arg	Gly	Val	Pro	Ser	Asn	Tyr	Val	Lys	Ala	Thr	Glu	Cys
145					150					155				160	
Phe	Arg	Lys	Ala	Met	His	Lys	Gly	Asn	Val	Glu	Ala	Tyr	Ile	Leu	Leu
			165					170						175	
Gly	Asp	Ile	Tyr	Tyr	Ser	Gly	Asn	Asp	Gln	Leu	Gly	Ile	Glu	Pro	Asp
		180					185						190		
Lys	Asp	Lys	Ala	Ile	Val	Tyr	Tyr	Lys	Met	Ala	Ala	Asp	Met	Ser	Ser
	195						200					205			
Ser	Arg	Ala	Tyr	Glu	Gly	Leu	Ala	Glu	Ser	Tyr	Gln	Tyr	Gly	Leu	Gly
	210					215					220				
Val	Glu	Lys	Asp	Lys	Lys	Lys	Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys
225				230						235				240	
Asp	Phe	Asp	Ile	Asp	Lys	Asn	Cys	Lys	Lys	Asn	Thr	Ser	Ser	Arg	
			245					250						255	

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 <211> 319

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (66)...(269)

<400> 301

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aggctc atg aat agt tct aat ctc aaa aat tgg cta ttc cct acc att tgc 110
Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys
1 5 10 15

ttt ttt tta ttt tgt tat att tta att ttt tta atg ttc ttt atg ttt 158
Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe
20 25 30

aaa agt ttg caa tcg caa tcg ttt ggc tct gtg gca gaa acc gga aaa 206
Lys Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys
35 40 45

aaa ccc atc acc acc acc aag aaa ttt ggt aag gaa ttg caa aaa cag 254
Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln
50 55 60

att tca aaa atc cat taactttttt tcttttttgc cgataacttgc tgtaatggaa 309
Ile Ser Lys Ile His
65

tgaatatcaa 319

<210> 302

<211> 68

<212> PRT

<213> Helicobacter pylori

<400> 302

Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys Phe
1 5 10 15
Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe Lys
20 25 30
Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys Lys
35 40 45
Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln Ile
50 55 60
Ser Lys Ile His
65

<210> 303

<211> 1112

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (66)...(1058)

<400> 303

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ctagg atg aaa agg ctt ttt ttt atc cct ttt atc gct ccc ttt ttt ctc 110

Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu
1 5 10 15

aat ggg gag cct tca gcg ttt gat ttg caa agt ggg gct acc aaa aaa 158
Asn Gly Glu Pro Ser Ala Phe Asp Leu Gln Ser Gly Ala Thr Lys Lys
20 25 30

gaa ctc aag cag ttg caa atc aat agt aag aat ttt tct aat att ttg 206
Glu Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu
35 40 45

acc aaa atc cat tcg caa gta gag gct aac act caa gct caa gag ggt 254
Thr Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly
50 55 60

ttg aga agc gtt tat gag ggg cag gct aat aag att aaa gat ctc aat 302
Leu Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn
65 70 75

aac gct atc ctt tcc caa gaa gaa tcc tta cga gcc tta aaa gct tcg 350
Asn Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser
80 85 90 95

caa gaa gtg cag gct aac acg ctt aag cag caa tcg caa act tta gag 398
Gln Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu
100 105 110

gat ttg agg aat gag att cac gct aac cag caa gct atc cag cag tta 446
Asp Leu Arg Asn Glu Ile His Ala Asn Gln Gln Ala Ile Gln Gln Leu
115 120 125

gac aag caa aat aaa gag atg agt gaa tta ttg acc aag tta agc cag 494
Asp Lys Gln Asn Lys Glu Met Ser Glu Leu Leu Thr Lys Leu Ser Gln
130 135 140

gat ttg gtt tca caa atc gcc tta atc caa aaa gct ctc aaa gaa caa 542
Asp Leu Val Ser Gln Ile Ala Leu Ile Gln Lys Ala Leu Lys Glu Gln
145 150 155

gag gaa aaa gct gaa aag ccg ctc aaa tca aac gct ccg gct aat aaa 590
Glu Glu Lys Ala Glu Lys Pro Leu Lys Ser Asn Ala Pro Ala Asn Lys
160 165 170 175

acc ccc tct ttg aaa gcc gaa tcc cca aaa aat caa gag gga aaa act 638
Thr Pro Ser Leu Lys Ala Glu Ser Pro Lys Asn Gln Glu Gly Lys Thr
180 185 190

caa gaa aag gcg aaa att gag ttt gat aaa gac ttg tct aag caa aaa 686
Gln Glu Lys Ala Lys Ile Glu Phe Asp Lys Asp Leu Ser Lys Gln Lys

195	200	205	
gag atc ttt caa gaa gct ctg tct ttt ttt aaa aat aaa tcc tat gca			734
Glu Ile Phe Gln Glu Ala Leu Ser Phe Phe Lys Asn Lys Ser Tyr Ala			
210	215	220	
gaa gcc aaa gag cgt ttg ttg tgg tta gaa gcc aat agt tac aga ctt			782
Glu Ala Lys Glu Arg Leu Leu Trp Leu Glu Ala Asn Ser Tyr Arg Leu			
225	230	235	
tat tat gtg cgt tat gtt ctt gga gaa gtg gct tat ggg gaa aag aga			830
Tyr Tyr Val Arg Tyr Val Leu Gly Glu Val Ala Tyr Gly Glu Lys Arg			
240	245	250	255
tac aga gaa gcg atc aag tat tac aaa gag agc gct ctt tta aac aaa			878
Tyr Arg Glu Ala Ile Lys Tyr Tyr Lys Glu Ser Ala Leu Leu Asn Lys			
260	265	270	
aaa gcg tct tac atg cct gtg ctt ttg tgg cat acg gca tgg tcg ttt			926
Lys Ala Ser Tyr Met Pro Val Leu Leu Trp His Thr Ala Trp Ser Phe			
275	280	285	
aaa aaa atc aaa gac gat caa aac tat tat aaa ttt tta aac act ttg			974
Lys Lys Ile Lys Asp Asp Gln Asn Tyr Tyr Lys Phe Leu Asn Thr Leu			
290	295	300	
caa cac ttg tat cct tca agc gaa caa gct aaa atg gcg caa aaa atc			1022
Gln His Leu Tyr Pro Ser Ser Glu Gln Ala Lys Met Ala Gln Lys Ile			
305	310	315	
tta gaa aac aag gag aaa cac cac cat gca aaa cca tgatttagag			1068
Leu Glu Asn Lys Glu Lys His His His Ala Lys Pro			
320	325	330	
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20 25 30			
Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu Thr			
35 40 45			
Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly Leu			
50 55 60			
Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn Asn			
65 70 75 80			
Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln			
85 90 95			
Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp			

35	40	45	50	
aaa acg gat aat gcc caa agt gtg gag att ggc cat caa att gag gct				249
Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile Glu Ala				
	55	60	65	
ctt ctt aaa gaa gcg gct gaa aaa cgc aga gaa ata ata gca gaa gcg				297
Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala Glu Ala				
	70	75	80	
att caa aaa gcc aca gag tcc tat gac gct gtg atc aag caa aaa gag				345
Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln Lys Glu				
	85	90	95	
aac gaa ctc aat caa gag ttt gaa gcg ttt gcg aag caa tta caa aat				393
Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu Gln Asn				
	100	105	110	
gaa aag caa gcg cta aaa gag cag ttg caa gcg caa atg ccg gta ttt				441
Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro Val Phe				
	115	120	125	130
gaa gac gag tta aac aag cgt gtg gct atg ggt tta ggg agt				483
Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser				
	135	140		
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<210> 306

<211> 144

<212> PRT

<213> Helicobacter pylori

<400> 306

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	20	25	30	
Leu Ala Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala				
	35	40	45	
Lys Ile Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile				
	50	55	60	
Glu Ala Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala				
	65	70	75	80
Glu Ala Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln				
	85	90	95	
Lys Glu Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu				
	100	105	110	
Gln Asn Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro				
	115	120	125	
Val Phe Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser				
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<210> 307

<211> 5832
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<220>
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<400> 307

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ataaagaagg cgatcaaadc cctaaagaag aaatcgcttc aatcaaccgc ttcacttttg 180
ctagtttggg caaaaagtat tctaaagaag tgcaaaacca ctatgaaatc actaaaaaca 240
atttcttaga gcaaaagaaa gttttgggcg aagagcatga agaaaagctt tctatttttag 300
aaaaagatga tattttgcct aatggcgtga tcaaaaaagt caagctctat atcgctacaa 360
aacgaaagct taaagtgggc gataaa atg gca gga agg cat ggg aat aaa ggg 413
Met Ala Gly Arg His Gly Asn Lys Gly
1 5
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att gtg tct aat atc gtg ccg gtt gcg gat atg cct tat acc gct gat 461
Ile Val Ser Asn Ile Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp
10 15 20 25
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ggc gag cct gta gat att gtt tta aac cct tta ggc gtg cca agc cgc 509
Gly Glu Pro Val Asp Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg
30 35 40
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atg aat atc ggg cag att tta gaa atg cat tta ggc tta gtg ggg aaa 557
Met Asn Ile Gly Gln Ile Leu Glu Met His Leu Gly Leu Val Gly Lys
45 50 55
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gaa ttt ggg aag caa atc gct cgc atg cta gag gat aaa acc aaa gat 605
Glu Phe Gly Lys Gln Ile Ala Arg Met Leu Glu Asp Lys Thr Lys Asp
60 65 70
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ttt gcc aaa gaa ttg cgt gct aaa atg cta gaa awc gct aac gct att 653
Phe Ala Lys Glu Leu Arg Ala Lys Met Leu Glu Xaa Ala Asn Ala Ile
75 80 85
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aat gaa aaa gac ccc ttg aca atc cat gcg ctt gag aat tgt tct gat 701
Asn Glu Lys Asp Pro Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp
90 95 100 105
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```
gaa gag ctt ttg gaa tac gca aaa gat tgg agc aag ggc gtt aag atg 749
Glu Glu Leu Leu Glu Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met
110 115 120
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gct atc cct gtg ttt gaa ggc atc tcg caa gaa aaa ttt tat aag cta 797
Ala Ile Pro Val Phe Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu
125 130 135
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ttt gaa tta gct aag atc gct atg gat ggc aaa atg gat ctg tat gac 845
Phe Glu Leu Ala Lys Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp
140 145 150
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gga cgc aca ggc gag aaa atg agg gag cgc gtg aat gtg ggc tac atg	893
Gly Arg Thr Gly Glu Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met	
155 160 165	
tat atg atc aaa ctc cac cat tta gtg gat gaa aaa gtc cat gcc aga	941
Tyr Met Ile Lys Leu His His Leu Val Asp Glu Lys Val His Ala Arg	
170 175 180 185	
agc aca ggc cct tat agc tta gta acg cac cag ccc gtg ggg ggt aaa	989
Ser Thr Gly Pro Tyr Ser Leu Val Thr His Gln Pro Val Gly Gly Lys	
190 195 200	
gcg ctc ttt ggg ggt caa agg ttt ggg gaa atg gaa gtg tgg gcc ttg	1037
Ala Leu Phe Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu	
205 210 215	
gaa gct tat ggc gca gcg cac act cta aaa gaa atg ctc acc att aaa	1085
Glu Ala Tyr Gly Ala Ala His Thr Leu Lys Glu Met Leu Thr Ile Lys	
220 225 230	
tcc gat gat att aga ggc aga gag aac gct tat agg gct atc gct aaa	1133
Ser Asp Asp Ile Arg Gly Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys	
235 240 245	
ggg gag caa gtg ggc gag agt gaa atc cct gag act ttc tat gtt ttg	1181
Gly Glu Gln Val Gly Glu Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu	
250 255 260 265	
act aaa gaa ttg caa tcg ctc gct ttg gat att aat att ttt ggg gac	1229
Thr Lys Glu Leu Gln Ser Leu Ala Leu Asp Ile Asn Ile Phe Gly Asp	
270 275 280	
gat gtg gat gag gat gga gca cct aaa ccc att gtc att aaa gaa gat	1277
Asp Val Asp Glu Asp Gly Ala Pro Lys Pro Ile Val Ile Lys Glu Asp	
285 290 295	
gac agg cct aaa gac ttt agc tct ttc cag ctc aca cta gct agc cct	1325
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300 305 310	
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Glu Lys Ile His Ser Trp Ser Tyr Gly Glu Val Lys Lys Pro Glu Thr	
315 320 325	
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Ile Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Cys Met	
330 335 340 345	
aaa atc ttt ggc ccc act aaa gat tat gaa tgc ttg tgc ggc aaa tac	1469
Lys Ile Phe Gly Pro Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr	
350 355 360	
aaa aag cct cgc ttc aaa gac att ggc aca tgc gaa aaa tgc ggc gtg	1517
Lys Lys Pro Arg Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val	
365 370 375	

gcg atc acg cac tcc aaa gtc agg cgt ttt aga atg ggg cat att gaa	1565
Ala Ile Thr His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu	
380 385 390	
ttg gcc act cct gta gcg cat atc tgg tat gtt aat tcc ttg cct agc	1613
Leu Ala Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser	
395 400 405	
cgt atc ggc acg ctt tta ggc gtt aag atg aaa gac tta gag cgc gtg	1661
Arg Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val	
410 415 420 425	
ttg tat tat gaa gct tat atc gtt aaa gaa cca ggc gaa gcc gct tat	1709
Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala Tyr	
430 435 440	
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Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu Asn Glu	
445 450 455	
gag cag tat caa aat atc tca cga aga tac gaa gac agg ggc ttt gta	1805
Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg Gly Phe Val	
460 465 470	
gcg caa atg ggc ggt gaa gcg atc aag gat ttg tta gaa gaa att gat	1853
Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu Glu Glu Ile Asp	
475 480 485	
ttg atc acc tta ttg cag agt ttg aaa gaa gaa gtg aaa gac acc aat	1901
Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu Val Lys Asp Thr Asn	
490 495 500 505	
tct gat gcg aaa aag aaa aaa ctc att aag cgt ttg aaa gtg gta gaa	1949
Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys Arg Leu Lys Val Val Glu	
510 515 520	
agc ttt tta aat tct ggt aat agg cct gaa tgg atg atg ctc acg gtt	1997
Ser Phe Leu Asn Ser Gly Asn Arg Pro Glu Trp Met Met Leu Thr Val	
525 530 535	
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Leu Pro Val Leu Pro Pro Asp Leu Arg Pro Leu Val Ala Leu Asp Gly	
540 545 550	
ggg aag ttt gca gtc agc gat gtg aat gaa ttg tat cgt cgt gtc atc	2093
Gly Lys Phe Ala Val Ser Asp Val Asn Glu Leu Tyr Arg Arg Val Ile	
555 560 565	
aat cgt aac caa cgc ttg aaa cgc tta atg gag ctt gga gcg cca gaa	2141
Asn Arg Asn Gln Arg Leu Lys Arg Leu Met Glu Leu Gly Ala Pro Glu	
570 575 580 585	
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Ile Ile Val Arg Asn Glu Lys Arg Met Leu Gln Glu Ala Val Asp Val	

590										595										600										
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Leu	Phe	Asp	Asn	Gly	Arg	Ser	Thr	Asn	Ala	Val	Lys	Gly	Ala	Asn	Lys															
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cgc	cct	tta	aaa	tcg	ctc	agt	gaa	atc	att	aaa	ggc	aag	cag	ggg	cgt	2285														
Arg	Pro	Leu	Lys	Ser	Leu	Ser	Glu	Ile	Ile	Lys	Gly	Lys	Gln	Gly	Arg															
620					625					630																				
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Phe	Arg	Gln	Asn	Leu	Leu	Gly	Lys	Arg	Val	Asp	Phe	Ser	Gly	Arg	Ser															
635					640					645																				
gtg	att	gtg	gtt	ggg	cct	aat	ctc	aaa	atg	gat	gaa	tgc	ggg	ttg	cct	2381														
Val	Ile	Val	Val	Gly	Pro	Asn	Leu	Lys	Met	Asp	Glu	Cys	Gly	Leu	Pro															
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aaa	aac	atg	gcg	tta	gaa	ctc	ttc	aaa	ccg	cat	ttg	tta	tcc	aag	ctt	2429														
Lys	Asn	Met	Ala	Leu	Glu	Leu	Phe	Lys	Pro	His	Leu	Leu	Ser	Lys	Leu															
670					675					680																				
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Glu	Glu	Arg	Gly	Tyr	Ala	Thr	Thr	Leu	Lys	Gln	Ala	Lys	Arg	Met	Ile															
685					690					695																				
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700					705					710																				
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Ile	Gln	Ala	Phe	His	Pro	Lys	Leu	Ile	Asp	Gly	Lys	Ala	Ile	Gln	Leu															
730					735					740					745															
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His	Pro	Leu	Val	Cys	Ser	Ala	Phe	Asn	Ala	Asp	Phe	Asp	Gly	Asp	Gln															
750					755					760																				
atg	gcg	gtg	cat	gtg	cct	tta	agc	cag	gaa	gcg	atc	gct	gaa	tgc	aag	2717														
Met	Ala	Val	His	Val	Pro	Leu	Ser	Gln	Glu	Ala	Ile	Ala	Glu	Cys	Lys															
765					770					775																				
gtg	ctg	atg	cta	agc	tct	atg	aat	atc	ctt	ttg	cct	gct	agc	ggt	aag	2765														
Val	Leu	Met	Leu	Ser	Ser	Met	Asn	Ile	Leu	Leu	Pro	Ala	Ser	Gly	Lys															
780					785					790																				
gcc	gta	gcc	att	cct	agc	caa	gat	atg	gtt	tta	ggg	ctt	tat	tat	ctt	2813														
Ala	Val	Ala	Ile	Pro	Ser	Gln	Asp	Met	Val	Leu	Gly	Leu	Tyr	Tyr	Leu															
795					800					805																				
tct	tta	gaa	aag	agc	ggg	gtc	aag	ggc	gag	cat	aag	ctt	ttt	tct	agc	2861														

Ser	Leu	Glu	Lys	Ser	Gly	Val	Lys	Gly	Glu	His	Lys	Leu	Phe	Ser	Ser		
810					815					820					825		
gtg	aat	gaa	atc	atc	acc	gcc	att	gac	acg	aaa	gaa	tta	gac	atc	cac	2909	
Val	Asn	Glu	Ile	Ile	Thr	Ala	Ile	Asp	Thr	Lys	Glu	Leu	Asp	Ile	His		
				830					835					840			
gca	aag	att	agg	gtt	tta	gat	caa	ggg	aat	att	atc	gct	acg	agt	gca	2957	
Ala	Lys	Ile	Arg	Val	Leu	Asp	Gln	Gly	Asn	Ile	Ile	Ala	Thr	Ser	Ala		
			845					850					855				
ggg	cgc	atg	atc	att	aag	tcc	att	ttg	cct	gat	ttt	atc	cct	acg	gat	3005	
Gly	Arg	Met	Ile	Ile	Lys	Ser	Ile	Leu	Pro	Asp	Phe	Ile	Pro	Thr	Asp		
		860					865					870					
ttg	tgg	aac	aga	ccc	atg	aag	aaa	aaa	gat	att	ggc	gtg	ctt	gtg	gat	3053	
Leu	Trp	Asn	Arg	Pro	Met	Lys	Lys	Lys	Asp	Ile	Gly	Val	Leu	Val	Asp		
	875					880					885						
tat	gtg	cat	aaa	gtt	ggc	ggg	atc	ggg	att	act	gca	acc	ttt	ttg	gat	3101	
Tyr	Val	His	Lys	Val	Gly	Gly	Ile	Gly	Ile	Thr	Ala	Thr	Phe	Leu	Asp		
890					895				900						905		
aat	tta	aaa	acg	ctt	ggc	ttt	agg	tat	gcg	act	aag	gct	ggg	att	tct	3149	
Asn	Leu	Lys	Thr	Leu	Gly	Phe	Arg	Tyr	Ala	Thr	Lys	Ala	Gly	Ile	Ser		
				910					915					920			
atc	tct	atg	gag	gat	att	atc	acg	cca	aaa	gac	aag	caa	aaa	atg	gtg	3197	
Ile	Ser	Met	Glu	Asp	Ile	Ile	Thr	Pro	Lys	Asp	Lys	Gln	Lys	Met	Val		
			925					930					935				
gaa	aaa	gcc	aaa	gta	gag	gtt	aaa	aaa	atc	cag	caa	caa	tac	gat	caa	3245	
Glu	Lys	Ala	Lys	Val	Glu	Val	Lys	Lys	Ile	Gln	Gln	Gln	Tyr	Asp	Gln		
		940					945					950					
ggg	ctg	ctc	act	gac	caa	gag	cgt	tac	aat	aag	atc	att	gac	act	tgg	3293	
Gly	Leu	Leu	Thr	Asp	Gln	Glu	Arg	Tyr	Asn	Lys	Ile	Ile	Asp	Thr	Trp		
	955					960					965						
act	gaa	gtc	aat	gac	aaa	atg	agt	aaa	gaa	atg	atg	acc	gct	atc	gcg	3341	
Thr	Glu	Val	Asn	Asp	Lys	Met	Ser	Lys	Glu	Met	Met	Thr	Ala	Ile	Ala		
970					975				980					985			
caa	gat	aaa	gag	ggc	ttt	aac	tct	att	tat	atg	atg	gca	gat	agc	ggc	3389	
Gln	Asp	Lys	Glu	Gly	Phe	Asn	Ser	Ile	Tyr	Met	Met	Ala	Asp	Ser	Gly		
				990					995					1000			
gca	agg	ggg	agc	gcg	gcg	caa	atc	cgt	cag	ctt	tca	gcg	atg	agg	ggg	3437	
Ala	Arg	Gly	Ser	Ala	Ala	Gln	Ile	Arg	Gln	Leu	Ser	Ala	Met	Arg	Gly		
			1005					1010					1015				
ctt	atg	aca	aag	ccg	gac	ggc	agt	atc	att	gaa	acg	ccc	att	att	tct	3485	
Leu	Met	Thr	Lys	Pro	Asp	Gly	Ser	Ile	Ile	Glu	Thr	Pro	Ile	Ile	Ser		
		1020					1025					1030					

aac ttt aaa gag ggg ttg aat gtc tta gaa tac ttc aat tcc acg cat	3533
Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His	
1035 1040 1045	
ggc gct aga aag ggc tta gcg gat aca gcg cta aaa aca gcc aat gcg	3581
Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala	
1050 1055 1060 1065	
ggg tat ttg acc aga aag ctc att gat gtt tcg caa aat gtc aag gtg	3629
Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val	
1070 1075 1080	
gtg tct gat gat tgc ggc acg cat gaa ggg att gaa atc acg gat att	3677
Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile	
1085 1090 1095	
gcg gtg ggg agt gag ctg att gaa cct tta gaa gag cgt att ttt ggg	3725
Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly	
1100 1105 1110	
cgc gtt tta tta gaa gat gtg atc gat ccc att acg aat gaa atc ttg	3773
Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu	
1115 1120 1125	
ctt tat gcg gac act ttg att gat gaa gag ggt gct aaa aag gtg gtt	3821
Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val	
1130 1135 1140 1145	
gaa gcc ggg att aaa tcc att acg atc cgc acc cca gta act tgt aaa	3869
Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys	
1150 1155 1160	
gcg cca aag ggc gtg tgc gcg aaa tgc tat ggc ttg aat ttg ggc gaa	3917
Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu	
1165 1170 1175	
ggc aag atg agt tat ccg ggt gaa gcg gtg ggc gtg gta gcc gcg caa	3965
Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln	
1180 1185 1190	
tct att ggg gag cct gga acg cag ctc act tta agg act ttc cat gtg	4013
Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val	
1195 1200 1205	
ggc ggg aca gcg agc agg agt cag gat gag cgc gaa atc gta gcg agc	4061
Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser	
1210 1215 1220 1225	
aaa gaa ggt ttt gtg cgt ttt tac aac ctt agg act tac acg aat aaa	4109
Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu Arg Thr Tyr Thr Asn Lys	
1230 1235 1240	
gag ggt aaa aac att atc gct aac cgc cgt aac gct tct att tta gtg	4157
Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val	
1245 1250 1255	

gta gag cct aag att aaa gcg cct ttt gat ggg gaa tta cgc att gaa	4205
Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu	
1260 1265 1270	
acg gtt tat gaa gaa gtc gtt gtg agc gtg aaa aat ggc gat caa gaa	4253
Thr Val Tyr Glu Glu Val Val Val Ser Val Lys Asn Gly Asp Gln Glu	
1275 1280 1285	
gct aaa ttt gtt tta agg aga agc gat att gtc aag cca agc gaa tta	4301
Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu	
1290 1295 1300 1305	
gcc ggc gtt ggc ggt aag att gag ggg aaa gtg tat ttg cct tat gct	4349
Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala	
1310 1315 1320	
agt ggg cat aag gtg cat aag ggg gga agt atc gct gat att atc caa	4397
Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln	
1325 1330 1335	
gag ggc tgg aat gtg cct aat cgc atc cct tat gcg agc gaa ttg cta	4445
Glu Gly Trp Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu	
1340 1345 1350	
gtc aag gat aat gac cct att gcg caa gat gtg tat gcc aaa gaa aaa	4493
Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys	
1355 1360 1365	
ggc gta atc aaa tac tat gtt tta gag gct aac cat tta gag cgc acc	4541
Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr	
1370 1375 1380 1385	
cat ggg atc aaa aag ggc gat atg gtg agt gaa aaa ggc ttg ttt gcg	4589
His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala	
1390 1395 1400	
gtg ata gct gat gat aat ggt agg gaa gcc gct cgc cat tat atc gct	4637
Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala	
1405 1410 1415	
agg ggt tct gag atc ttg att gat gat aat agt gaa gtg agc act aat	4685
Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn	
1420 1425 1430	
agc gtg att tct aaa ccc acg act aac act ttc aaa acg att gcc aca	4733
Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys Thr Ile Ala Thr	
1435 1440 1445	
tgg gat cct tac aac acc cct atc att gcg gac ttt aaa ggt aag gtg	4781
Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val	
1450 1455 1460 1465	
ggt ttt gtg gat gtt atc gca ggg gtt acg gtc gct gaa aaa gaa gac	4829
Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp	

1470	1475	1480	
gaa aat acc ggt atc aca agc tta gtg	gtg aat gat tac att cca agc	4877	
Glu Asn Thr Gly Ile Thr Ser Leu Val	Val Asn Asp Tyr Ile Pro Ser		
1485	1490 1495		
gga tac aaa cca agc ttg ttt tta gag	ggg gct aat ggc gaa gag atg	4925	
Gly Tyr Lys Pro Ser Leu Phe Leu Glu	Gly Ala Asn Gly Glu Glu Met		
1500	1505 1510		
cgt tat ttc cta gag cca aaa acc tct	atc gcc att agc gat ggc tct	4973	
Arg Tyr Phe Leu Glu Pro Lys Thr Ser	Ile Ala Ile Ser Asp Gly Ser		
1515	1520 1525		
agc gtg gag caa gct gaa gtg tta gcg	aaa atc cct aaa gcg acc gtt	5021	
Ser Val Glu Gln Ala Glu Val Leu Ala	Lys Ile Pro Lys Ala Thr Val		
1530	1535 1540 1545		
aaa tct agg gat att acc ggg ggt ctc	cca agg gtt tcg gaa ctc ttt	5069	
Lys Ser Arg Asp Ile Thr Gly Gly Leu	Pro Arg Val Ser Glu Leu Phe		
1550	1555 1560		
gaa gcg aga aaa ccc aag cct aaa gat	gtg gcg atc ctt tct gaa gtt	5117	
Glu Ala Arg Lys Pro Lys Pro Lys Asp	Val Ala Ile Leu Ser Glu Val		
1565	1570 1575		
gat ggg att gtg agt ttt ggc aaa ccc	att cgc aat aaa gaa cac atc	5165	
Asp Gly Ile Val Ser Phe Gly Lys Pro	Ile Arg Asn Lys Glu His Ile		
1580	1585 1590		
atc gta act tct aaa gat ggc cgt tcc	atg gat tat ttt gtg gat aaa	5213	
Ile Val Thr Ser Lys Asp Gly Arg Ser	Met Asp Tyr Phe Val Asp Lys		
1595	1600 1605		
ggc aag caa att tta gtg cat gcc gat	gaa ttt gtg cat gcg gga gaa	5261	
Gly Lys Gln Ile Leu Val His Ala Asp	Glu Phe Val His Ala Gly Glu		
1610	1615 1620 1625		
gcg atg acg gac gga gta att tca agc	cat gat att tta agg atc agt	5309	
Ala Met Thr Asp Gly Val Ile Ser Ser	His Asp Ile Leu Arg Ile Ser		
1630	1635 1640		
ggc gaa aaa gag ctt tat aaa tac att	gtg agc gaa gtc cag caa gtg	5357	
Gly Glu Lys Glu Leu Tyr Lys Tyr Ile	Val Ser Glu Val Gln Gln Val		
1645	1650 1655		
tat cgc agg cag ggg gtg agc att gcg	gac aag cac att gaa atc att	5405	
Tyr Arg Arg Gln Gly Val Ser Ile Ala	Asp Lys His Ile Glu Ile Ile		
1660	1665 1670		
gtt tct caa atg cta aga cag gtg cgt	att tta gac agc ggg gat agc	5453	
Val Ser Gln Met Leu Arg Gln Val Arg	Ile Leu Asp Ser Gly Asp Ser		
1675	1680 1685		
aag ttt att gaa ggg gat tta gtc agt	aaa aaa ctt ttc aaa gaa gaa	5501	

Lys Phe Ile Glu Gly Asp Leu Val Ser Lys Lys Leu Phe Lys Glu Glu
 1690 1695 1700 1705
 aac gct cgt gtg atc gct tta aaa ggc gag cca gcg att gct gaa ccg 5549
 Asn Ala Arg Val Ile Ala Leu Lys Gly Glu Pro Ala Ile Ala Glu Pro
 1710 1715 1720
 gtg ctt tta ggg atc act aga gcg gct att ggg agc gat agc atc atc 5597
 Val Leu Leu Gly Ile Thr Arg Ala Ala Ile Gly Ser Asp Ser Ile Ile
 1725 1730 1735
 tca gcg gcc tct ttc caa gaa acg act aaa gtt tta aca gaa gcc agt 5645
 Ser Ala Ala Ser Phe Gln Glu Thr Lys Val Leu Thr Glu Ala Ser
 1740 1745 1750
 atc gct atg aaa aaa gac ttt tta gag gat ttg aaa gag aat gtg gtg 5693
 Ile Ala Met Lys Lys Asp Phe Leu Glu Asp Leu Lys Glu Asn Val Val
 1755 1760 1765
 ttg ggg agg atg atc cct gtg gga aca ggc atg tat aag aat aaa aaa 5741
 Leu Gly Arg Met Ile Pro Val Gly Thr Gly Met Tyr Lys Asn Lys Lys
 1770 1775 1780 1785
 atc gtg tta aga gcg ctt gag gat aac tct aaa ttt tgatatgaaa 5787
 Ile Val Leu Arg Ala Leu Glu Asp Asn Ser Lys Phe
 1790 1795

aatcgggttaa gattttttaa agaaaaatta gggtaaaatg gggga 5832

<210> 308

<211> 1797

<212> PRT

<213> *Helicobacter pylori*

<220>

<221> VARIANT

<222> 85

<223> Xaa = Any Amino Acid

<400> 308

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 20 25 30
 Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu
 35 40 45
 Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala
 50 55 60
 Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala
 65 70 75 80
 Lys Met Leu Glu Xaa Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu Thr
 85 90 95
 Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu Tyr Ala
 100 105 110
 Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe Glu Gly

Val	Asn	Glu	Leu	Tyr	Arg	Arg	Val	Ile	Asn	Arg	Asn	Gln	Arg	Leu	Lys	565	570	575
Arg	Leu	Met	Glu	Leu	Gly	Ala	Pro	Glu	Ile	Ile	Val	Arg	Asn	Glu	Lys	580	585	590
Arg	Met	Leu	Gln	Glu	Ala	Val	Asp	Val	Leu	Phe	Asp	Asn	Gly	Arg	Ser	595	600	605
Thr	Asn	Ala	Val	Lys	Gly	Ala	Asn	Lys	Arg	Pro	Leu	Lys	Ser	Leu	Ser	610	615	620
Glu	Ile	Ile	Lys	Gly	Lys	Gln	Gly	Arg	Phe	Arg	Gln	Asn	Leu	Leu	Gly	625	630	635
Lys	Arg	Val	Asp	Phe	Ser	Gly	Arg	Ser	Val	Ile	Val	Val	Gly	Pro	Asn	645	650	655
Leu	Lys	Met	Asp	Glu	Cys	Gly	Leu	Pro	Lys	Asn	Met	Ala	Leu	Glu	Leu	660	665	670
Phe	Lys	Pro	His	Leu	Leu	Ser	Lys	Leu	Glu	Glu	Arg	Gly	Tyr	Ala	Thr	675	680	685
Thr	Leu	Lys	Gln	Ala	Lys	Arg	Met	Ile	Glu	Gln	Lys	Ser	Asn	Glu	Val	690	695	700
Trp	Glu	Cys	Leu	Gln	Glu	Ile	Thr	Glu	Gly	Tyr	Pro	Val	Leu	Leu	Asn	705	710	715
Arg	Ala	Pro	Thr	Leu	His	Lys	Gln	Ser	Ile	Gln	Ala	Phe	His	Pro	Lys	725	730	735
Leu	Ile	Asp	Gly	Lys	Ala	Ile	Gln	Leu	His	Pro	Leu	Val	Cys	Ser	Ala	740	745	750
Phe	Asn	Ala	Asp	Phe	Asp	Gly	Asp	Gln	Met	Ala	Val	His	Val	Pro	Leu	755	760	765
Ser	Gln	Glu	Ala	Ile	Ala	Glu	Cys	Lys	Val	Leu	Met	Leu	Ser	Ser	Met	770	775	780
Asn	Ile	Leu	Leu	Pro	Ala	Ser	Gly	Lys	Ala	Val	Ala	Ile	Pro	Ser	Gln	785	790	795
Asp	Met	Val	Leu	Gly	Leu	Tyr	Tyr	Leu	Ser	Leu	Glu	Lys	Ser	Gly	Val	805	810	815
Lys	Gly	Glu	His	Lys	Leu	Phe	Ser	Ser	Val	Asn	Glu	Ile	Ile	Thr	Ala	820	825	830
Ile	Asp	Thr	Lys	Glu	Leu	Asp	Ile	His	Ala	Lys	Ile	Arg	Val	Leu	Asp	835	840	845
Gln	Gly	Asn	Ile	Ile	Ala	Thr	Ser	Ala	Gly	Arg	Met	Ile	Ile	Lys	Ser	850	855	860
Ile	Leu	Pro	Asp	Phe	Ile	Pro	Thr	Asp	Leu	Trp	Asn	Arg	Pro	Met	Lys	865	870	875
Lys	Lys	Asp	Ile	Gly	Val	Leu	Val	Asp	Tyr	Val	His	Lys	Val	Gly	Gly	885	890	895
Ile	Gly	Ile	Thr	Ala	Thr	Phe	Leu	Asp	Asn	Leu	Lys	Thr	Leu	Gly	Phe	900	905	910
Arg	Tyr	Ala	Thr	Lys	Ala	Gly	Ile	Ser	Ile	Ser	Met	Glu	Asp	Ile	Ile	915	920	925
Thr	Pro	Lys	Asp	Lys	Gln	Lys	Met	Val	Glu	Lys	Ala	Lys	Val	Glu	Val	930	935	940
Lys	Lys	Ile	Gln	Gln	Gln	Tyr	Asp	Gln	Gly	Leu	Leu	Thr	Asp	Gln	Glu	945	950	955
Arg	Tyr	Asn	Lys	Ile	Ile	Asp	Thr	Trp	Thr	Glu	Val	Asn	Asp	Lys	Met	965	970	975
Ser	Lys	Glu	Met	Met	Thr	Ala	Ile	Ala	Gln	Asp	Lys	Glu	Gly	Phe	Asn	980	985	990
Ser	Ile	Tyr	Met	Met	Ala	Asp	Ser	Gly	Ala	Arg	Gly	Ser	Ala	Ala	Gln			

Thr Asn Thr Phe Lys Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro
 1445 1450 1455
 Ile Ile Ala Asp Phe Lys Gly Lys Val Gly Phe Val Asp Val Ile Ala
 1460 1465 1470
 Gly Val Thr Val Ala Glu Lys Glu Asp Glu Asn Thr Gly Ile Thr Ser
 1475 1480 1485
 Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe
 1490 1495 1500
 Leu Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys
 1505 1510 1515 1520
 Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val
 1525 1530 1535
 Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile Thr Gly
 1540 1545 1550
 Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys Pro Lys Pro
 1555 1560 1565
 Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile Val Ser Phe Gly
 1570 1575 1580
 Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val Thr Ser Lys Asp Gly
 1585 1590 1595 1600
 Arg Ser Met Asp Tyr Phe Val Asp Lys Gly Lys Gln Ile Leu Val His
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 Ala Asp Glu Phe Val His Ala Gly Glu Ala Met Thr Asp Gly Val Ile
 1620 1625 1630
 Ser Ser His Asp Ile Leu Arg Ile Ser Gly Glu Lys Glu Leu Tyr Lys
 1635 1640 1645
 Tyr Ile Val Ser Glu Val Gln Gln Val Tyr Arg Arg Gln Gly Val Ser
 1650 1655 1660
 Ile Ala Asp Lys His Ile Glu Ile Ile Val Ser Gln Met Leu Arg Gln
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 Val Arg Ile Leu Asp Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu
 1685 1690 1695
 Val Ser Lys Lys Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu
 1700 1705 1710
 Lys Gly Glu Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg
 1715 1720 1725
 Ala Ala Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu
 1730 1735 1740
 Thr Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe
 1745 1750 1755 1760
 Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro Val
 1765 1770 1775
 Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala Leu Glu
 1780 1785 1790
 Asp Asn Ser Lys Phe
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<220>
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<400> 309

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agga atg aaa act gag atg aaa tct tct tta aaa ctt ttt atg cgg cct 109
    Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro
      1              5              10              15

ttg ttg gtg gtt tta gcg ttc atg ttg ttg tat gct tta gtg cat gct 157
Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala
      20              25              30

gcg ctt ggt ttt tat gta aaa aaa gac agc gct cca ata agc cca aat 205
Ala Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn
      35              40              45

gta gaa aaa acc gag aca gag cgt caa aac ggc gtg ctt tcg ccc aaa 253
Val Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys
      50              55              60

caa gaa gaa gcc aac gca acc aca act gcc aca gaa gaa agc ccc acc 301
Gln Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr
      65              70              75

aaa gac aca gcg ccg cct tta gac aca gcc gcg caa aaa caa gaa act 349
Lys Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr
      80              85              90              95

aaa caa gag caa gaa aaa gaa aac gag cct aaa caa gat agc gtc ccg 397
Lys Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro
      100             105             110

ccc gtt caa aac aat caa aaa acc cct aca acc ccc tta atg gga aaa 445
Pro Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys
      115             120             125

aaa cct tta gag tat aaa gtc gca gtc agt ggc gtg aat gtg cgc gct 493
Lys Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala
      130             135             140

ttt ccc agc aca aaa ggt aaa atc ttg gga ttg ctt tta aaa aat aaa 541
Phe Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys
      145             150             155

agc gtg aaa gtt tta gaa atc caa aac gat tgg gct gaa att gaa ttt 589
Ser Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe
      160             165             170             175

tct cac gaa aca aag ggc tat gtg ttt tta aaa ctt tta aaa aag gct 637
Ser His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala
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Glu
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 35 40 45
 Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys Gln
 50 55 60
 Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr Lys
 65 70 75 80
 Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr Lys
 85 90 95
 Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro Pro
 100 105 110
 Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys Lys
 115 120 125
 Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe
 130 135 140
 Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Lys Asn Lys Ser
 145 150 155 160
 Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe Ser
 165 170 175
 His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala Glu
 180 185 190

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<220>
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 Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn
 1 5 10 15
 cct ctt caa gcc ctt gtg atc gag ctt tta gaa gaa atc aaa act tcg 158
 Pro Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser
 20 25 30
 ccg cat aaa ggc act ttt aag gct aaa gtc ctt gat tct aaa aaa cca 206

Pro	His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Lys	Pro		
			35					40					45				
aga	caa	gtt	tta	ggc	gtt	tat	aat	atc	tcc	cca	cac	aaa	aaa	ctc	acg	254	
Arg	Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr		
		50					55					60					
ctc	act	atc	acc	cac	ata	tcc	act	gca	atc	gtc	tat	caa	ccc	ctt	gat	302	
Leu	Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp		
		65				70					75						
gaa	aaa	ctt	tct	tta	gaa	aca	acc	tta	aac	cct	aac	cgc	cct	act	atc	350	
Glu	Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Asn	Pro	Asn	Arg	Pro	Thr	Ile		
80					85				90						95		
cct	aga	aac	acc	cag	att	gtt	ttt	tct	tca	aaa	gaa	ttg	aaa	gag	tcg	398	
Pro	Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Ser		
			100					105					110				
cac	ccg	cac	caa	atg	cct	tct	tta	aac	gcg	ccc	atg	caa	aaa	cca	caa	446	
His	Pro	His	Gln	Met	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln		
			115					120					125				
aac	aaa	ccc	cat	tca	tcg	caa	caa	cct	tct	caa	aac	ttt	tct	tac	cca	494	
Asn	Lys	Pro	His	Ser	Ser	Gln	Gln	Pro	Ser	Gln	Asn	Phe	Ser	Tyr	Pro		
		130					135					140					
gag	ccc	aaa	cta	ggc	tct	aaa	aac	tct	aaa	aac	agc	ctt	tta	cag	cct	542	
Glu	Pro	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro		
	145				150					155							
tta	gca	att	cct	agc	aaa	ata	agt	ccc	act	aac	gaa	act	caa	acg	cca	590	
Leu	Ala	Ile	Pro	Ser	Lys	Ile	Ser	Pro	Thr	Asn	Glu	Thr	Gln	Thr	Pro		
160					165				170						175		
aca	aac	gac	act	aaa	ccc	cct	tta	aag	cat	tct	tca	gaa	gat	caa	gaa	638	
Thr	Asn	Asp	Thr	Lys	Pro	Pro	Leu	Lys	His	Ser	Ser	Glu	Asp	Gln	Glu		
			180					185					190				
agc	aac	ctc	ttt	ata	acg	cca	ccc	act	gaa	aaa	acg	ctc	cct	aac	aac	686	
Ser	Asn	Leu	Phe	Ile	Thr	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn		
		195						200					205				
acc	tct	aac	gct	gat	att	agt	gaa	aac	aat	gaa	agc	aat	gag	aat	aaa	734	
Thr	Ser	Asn	Ala	Asp	Ile	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Lys		
		210					215					220					
gat	aat	gtg	gaa	aaa	caa	gcc	att	aga	gat	gct	aat	att	aaa	gaa	ttt	782	
Asp	Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Ala	Asn	Ile	Lys	Glu	Phe		
	225				230						235						
gca	tgc	ggg	aag	tgg	gtc	tat	gac	gat	gaa	aat	tta	caa	gcc	tac	cgc	830	
Ala	Cys	Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg		
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Pro Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp	
260 265 270	
att acc cct tgc gat tac agc acc gct gaa aat aaa agc ggt aaa atc	926
Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile	
275 280 285	
att acc ccc tat act aaa atc tcc gtt cat aaa aca gag cct tta gaa	974
Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu	
290 295 300	
gag cca caa act ttt gaa gct aaa aat aat ttc gcc att ctt caa gcc	1022
Glu Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala	
305 310 315	
aga agc tct aca gaa aaa tgc aaa agg gct aga gca aga aaa gac ggc	1070
Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly	
320 325 330 335	
acg act agg caa tgc tat cta ata gaa gag cct tta aaa caa gca tgg	1118
Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp	
340 345 350	
gag agt gag tat gaa atc acc acg caa tta gtg aaa gcc att tat gag	1166
Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu	
355 360 365	
cgc ccc aaa caa gac gat caa gta gag ccg act ttt tat gaa acc agc	1214
Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser	
370 375 380	
gaa ttg gct tat tct tcc aca cga aaa agc gaa ata acg cac aat gaa	1262
Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu	
385 390 395	
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Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly	
400 405 410 415	
cat tat tta aac gat ata att aaa gag agc agt gaa tat aaa gaa tgg	1358
His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp	
420 425 430	
gtt aaa aac cat gtg cgc ttt aaa gaa ggg gtg tgc atg gct tta gaa	1406
Val Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu	
435 440 445	
ata gaa gaa cag cca cga gct aaa agc acg cct ttg agt att gaa aac	1454
Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn	
450 455 460	
tct cgt gtg gta tgt gtc aaa aag ggg aat tat tta ttc aac gaa gtt	1502
Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val	
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1550

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<211> 479

<212> PRT

<213> Helicobacter pylori

<400> 312

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			20					25					30		
His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Lys	Pro	Arg
		35					40					45			
Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr	Leu
	50					55					60				
Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp	Glu
65				70						75				80	
Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Asn	Pro	Asn	Arg	Pro	Thr	Ile	Pro
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Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Ser	His
			100					105					110		
Pro	His	Gln	Met	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	Asn
		115					120					125			
Lys	Pro	His	Ser	Ser	Gln	Gln	Pro	Ser	Gln	Asn	Phe	Ser	Tyr	Pro	Glu
	130					135					140				
Pro	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	Leu
145				150						155				160	
Ala	Ile	Pro	Ser	Lys	Ile	Ser	Pro	Thr	Asn	Glu	Thr	Gln	Thr	Pro	Thr
				165					170					175	
Asn	Asp	Thr	Lys	Pro	Pro	Leu	Lys	His	Ser	Ser	Glu	Asp	Gln	Glu	Ser
			180					185					190		
Asn	Leu	Phe	Ile	Thr	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	Thr
		195					200					205			
Ser	Asn	Ala	Asp	Ile	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Lys	Asp
	210					215					220				
Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Ala	Asn	Ile	Lys	Glu	Phe	Ala
225				230						235				240	
Cys	Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg	Pro
				245					250					255	
Ser	Ile	Leu	Lys	Arg	Val	Asp	Glu	Asp	Lys	Gln	Thr	Ala	Thr	Asp	Ile
			260					265					270		
Thr	Pro	Cys	Asp	Tyr	Ser	Thr	Ala	Glu	Asn	Lys	Ser	Gly	Lys	Ile	Ile
		275					280					285			
Thr	Pro	Tyr	Thr	Lys	Ile	Ser	Val	His	Lys	Thr	Glu	Pro	Leu	Glu	Glu
	290					295					300				
Pro	Gln	Thr	Phe	Glu	Ala	Lys	Asn	Asn	Phe	Ala	Ile	Leu	Gln	Ala	Arg
305				310						315				320	
Ser	Ser	Thr	Glu	Lys	Cys	Lys	Arg	Ala	Arg	Ala	Arg	Lys	Asp	Gly	Thr
				325					330					335	
Thr	Arg	Gln	Cys	Tyr	Leu	Ile	Glu	Glu	Pro	Leu	Lys	Gln	Ala	Trp	Glu
			340				345					350			
Ser	Glu	Tyr	Glu	Ile	Thr	Thr	Gln	Leu	Val	Lys	Ala	Ile	Tyr	Glu	Arg
		355					360					365			

Pro	Lys	Gln	Asp	Asp	Gln	Val	Glu	Pro	Thr	Phe	Tyr	Glu	Thr	Ser	Glu
370						375					380				
Leu	Ala	Tyr	Ser	Ser	Thr	Arg	Lys	Ser	Glu	Ile	Thr	His	Asn	Glu	Leu
385						390					395				400
Asn	Leu	Asn	Glu	Lys	Phe	Met	Glu	Phe	Val	Glu	Val	Tyr	Glu	Gly	His
				405					410					415	
Tyr	Leu	Asn	Asp	Ile	Ile	Lys	Glu	Ser	Ser	Glu	Tyr	Lys	Glu	Trp	Val
			420					425					430		
Lys	Asn	His	Val	Arg	Phe	Lys	Glu	Gly	Val	Cys	Met	Ala	Leu	Glu	Ile
		435					440					445			
Glu	Glu	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser
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Arg	Val	Val	Cys	Val	Lys	Lys	Gly	Asn	Tyr	Leu	Phe	Asn	Glu	Val	
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 Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu
 1 5 10

gct agt gtt aca gct ata ggg gct ata gcg agt ctg gta gcg atg aaa 157
 Ala Ser Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys
 15 20 25 30

aag act tgg gat ccg ctt cca agc gtt gtt tca gcc ggt ttt acg acc 205
 Lys Thr Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr
 35 40 45

ata gat gtg gcg aat atg caa gaa ggg cag ttt tcc acc gtg gaa tgg 253
 Ile Asp Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp
 50 55 60

cgt ggg aaa ccg gtc tat atc ctc aag cgt tct aaa aaa gag ggc ttt 301
 Arg Gly Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe
 65 70 75

aat gaa aag cgc gat ttt aaa gtt ggc gag agc gtt ttt acc aca gcc 349
 Asn Glu Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala
 80 85 90

att caa att tgc acg cat tta ggg tgt atc ccc act tat caa gat gaa 397
 Ile Gln Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu
 95 100 105 110

gaa aaa ggc ttt tta tgc cca tgc cat ggg ggg cgt ttc act tct gat 445
 Glu Lys Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp
 115 120 125

 ggc gtg aat att gcc ggc act ccc cct cca cgc cct ttt gat atc ccg 493
 Gly Val Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro
 130 135 140

 cct ttt aaa att gaa ggc act aag atc act ttt ggt gaa gcc ggg gct 541
 Pro Phe Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala
 145 150 155

 gaa tac aag aaa atg atg gct aaa gcg taaggagagt ttaatggcag 588
 Glu Tyr Lys Lys Met Met Ala Lys Ala
 160 165

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 <212> PRT
 <213> Helicobacter pylori

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 Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr Ile Asp
 35 40 45
 Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp Arg Gly
 50 55 60
 Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe Asn Glu
 65 70 75 80
 Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala Ile Gln
 85 90 95
 Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu Glu Lys
 100 105 110
 Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp Gly Val
 115 120 125
 Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro Pro Phe
 130 135 140
 Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala Glu Tyr
 145 150 155 160
 Lys Lys Met Met Ala Lys Ala
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<222> (52)...(1167)

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Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr
      5                      10                      15

ctt tta ttg gct tct tta ggc cat gcg aaa atg gct ttt gaa tcc gat 153
Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp
      20                      25                      30

att gac acc aaa gcg cta gag gct ttt ggg gtt aat gcg ggc ttt tta 201
Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu
      35                      40                      45                      50

tcc caa atg ccc aac gct tta aaa aaa atg aat aaa gaa gaa gaa tgg 249
Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp
      55                      60                      65

aag aga ctt gtc aaa aga ttt gat gtg aat tac cag ttc atc ccc atc 297
Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile
      70                      75                      80

att aaa aac atg ctc ata gaa gcg agc gtg ccg caa gaa ttt tta ttt 345
Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe
      85                      90                      95

tta gcc atg gcc gag tct aaa ttt tca tca agg gct tat agc agg aaa 393
Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser Arg Lys
      100                      105                      110

aaa gcg gta ggg att tgg caa ttc atg cca agc acg gct aaa gaa tta 441
Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys Glu Leu
      115                      120                      125                      130

ggg ctt aag gtc aat cat tac att gat gaa aga aga gat ccc att aaa 489
Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro Ile Lys
      135                      140                      145

agc act caa gcg gcg atc act tat ttg aaa cgg ctc tac aag caa acc 537
Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys Gln Thr
      150                      155                      160

gga gag tgg tat ttg gtc gct atg gcg tat aat tac ggc tta cgc aag 585
Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu Arg Lys
      165                      170                      175

gtt caa aac gct att aaa gcc gcc ggc act tcg gac att aaa att ttg 633
Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys Ile Leu
      180                      185                      190
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Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu Tyr Ile	
195 200 205 210	
cgc tcc att cta agc cta gcg tta aaa ttc aac agc cta gac aac ctc	729
Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp Asn Leu	
215 220 225	
aaa gat aaa gaa tat ctg ctc aat cgt ggg gcg agg gtg agt tta gtg	777
Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser Leu Val	
230 235 240	
ggc gtc ccg ttt aaa agg cgt gct tct tta gtc caa gta gcc aaa aat	825
Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala Lys Asn	
245 250 255	
ttg aat ttg agt ttg gaa acc tta aaa tcc tac aac cac caa ttc cgt	873
Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln Phe Arg	
260 265 270	
tat aac att ctg cct tct aaa gac ccc act tat acc att tat atc cct	921
Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr Ile Pro	
275 280 285 290	
tat gaa aaa ctc gct ctt ttc aaa caa cgc cag atc aaa caa aat aaa	969
Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln Asn Lys	
295 300 305	
aac att caa gcc agt tca aaa agc cct ttt atc acc cat gtg gtc tta	1017
Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val Val Leu	
310 315 320	
cct aaa gaa acc cta tct tct atc gct aaa cgc tat caa gtc agt att	1065
Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val Ser Ile	
325 330 335	
tcc aat atc caa tta gcc aat gat ctc aaa gat tct aat att ttt atc	1113
Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile Phe Ile	
340 345 350	
cac cag cgt tta atc atc ccc acc aac aaa aaa tta ctc gct aca agg	1161
His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala Thr Arg	
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Glu Phe	
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Ser Asp Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly
          35          40          45
Phe Leu Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu
          50          55          60
Glu Trp Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile
65          70          75          80
Pro Ile Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe
          85          90          95
Leu Phe Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser
          100          105          110
Arg Lys Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys
          115          120          125
Glu Leu Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro
          130          135          140
Ile Lys Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys
145          150          155          160
Gln Thr Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu
          165          170          175
Arg Lys Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys
          180          185          190
Ile Leu Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu
          195          200          205
Tyr Ile Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp
          210          215          220
Asn Leu Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser
225          230          235          240
Leu Val Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala
          245          250          255
Lys Asn Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln
          260          265          270
Phe Arg Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr
          275          280          285
Ile Pro Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln
          290          295          300
Asn Lys Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val
305          310          315          320
Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val
          325          330          335
Ser Ile Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile
          340          345          350
Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala
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Thr Arg Glu Phe
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<213> Helicobacter pylori

<220>

<221> CDS

<222> (46)...(510)

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Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met Phe Gln Tyr Ala
5 10 15 20

ttc gct aaa agt ttg caa aaa cac tct aat acg cct gtg ctg tta gat 153
Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro Val Leu Leu Asp
25 30 35

atc act tct ttt gat tgg agc gat agg aaa atg caa tta gaa ctt ttc 201
Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln Leu Glu Leu Phe
40 45 50

cct att gat ttg ccc tat gcg agc gcg aaa gaa atc gct ata gct aaa 249
Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile Ala Ile Ala Lys
55 60 65

atg caa cac ctc ccc aag cta gta aga gac gcg ctc aaa tgc atg gga 297
Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu Lys Cys Met Gly
70 75 80

ttt gat agg gtg agt caa gaa atc gtt ttt gaa tac gag cct aaa ttg 345
Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr Glu Pro Lys Leu
85 90 95 100

cta aag cca agc cgc ttg act tat ttt ttt ggc tat ttc caa gat cca 393
Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr Phe Gln Asp Pro
105 110 115

cga tac ttt gat gct ata tcc cct tta atc aag caa acc ttc act cta 441
Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln Thr Phe Thr Leu
120 125 130

ccc ccc ccc ccc ccg aaa ata ata aga ata ata aaa aag agg aag 489
Pro Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile Lys Lys Arg Lys
135 140 145

aat atc agt gca agc ttt ctt tgatttttagc cgctaaaaac agcgtgtttg 540
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150 155

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<211> 155

<212> PRT

<213> Helicobacter pylori

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35 40 45
Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile
50 55 60
Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu
65 70 75 80
Lys Cys Met Gly Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr
85 90 95
Glu Pro Lys Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr
100 105 110
Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln
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Glu Thr Leu Ala Pro Phe Ser Ala Phe Ser Ser Leu Glu Phe Leu Asp
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Ile Ser Thr Pro Asn Leu His Ala Thr Pro Ile Glu Pro Ser Ala Ile
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Arg Phe Ser Lys Met Val Met Cys Arg Leu Phe Leu Ala Ser Leu Phe
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Gly Ala Ala Lys Asp Phe Ala Ser Asp Lys Ser Pro Lys His Phe Gln
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 <211> 496
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (77)...(445)

<400> 323
 atttagttca agagctttta gaagaatttt tgcaaagcgg ggctaaagag attttagaaa 60
 aggcgcagtt gtttta atg cgt ttg ttt atc gcg cta gtt ttg ttt tgg tgg 112
 Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp

	1	5	10	
tgg tta agc ttg aac gct aaa gaa gcg gat ttt atc tct gat tta gaa				160
Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu				
	15	20	25	
tac ggg atg gct ctt tat aaa aac cct agg ggt gtt gcg tgc gcg aaa				208
Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys				
	30	35	40	
tgc cat ggc att aaa ggc gaa caa caa gaa atc acc ttt tat tat gaa				256
Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu				
	45	50	55	60
aaa ggc gag aaa aaa atc ctc tac gcc cct aaa atc aac cat ttg gat				304
Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp				
	65	70	75	
ttt aaa acc ttt aaa gac gcc ttg agt tta ggc aaa ggc atg atg cct				352
Phe Lys Thr Phe Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro				
	80	85	90	
aaa tac aat ctc aat tta gaa gaa atc caa gcg att tat ctt tat atc				400
Lys Tyr Asn Leu Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile				
	95	100	105	
atc tct tta gag cat aaa gaa gag cgt aag gat tct cct aag cct				445
Ile Ser Leu Glu His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro				
	110	115	120	
taatcaaagc gcttgattta tgctaaaatg gagcgttgca tttttgtttt g				496

<210> 324

<211> 123

<212> PRT

<213> Helicobacter pylori

<400> 324

Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp Trp Leu Ser Leu				
1	5	10	15	
Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala				
	20	25	30	
Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile				
	35	40	45	
Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys				
	50	55	60	
Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe				
	65	70	75	80
Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu				
	85	90	95	
Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Ile Ser Leu Glu				
	100	105	110	
His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro				
	115	120		

<210> 325
 <211> 521
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (72)...(464)

<400> 325
 gttgcaacaa aaaatagaga gcaggaaaac agacattgtg atccaatcca tggcgaatat 60
 tctcagcggg a atg aat gag ctt atc cgc tat ggc ttg ata ttt ctc ttt 110
 1 5 10
 Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe
 ttt tta aag gcg ttt ggg ctt gat tat ggg ata gat aaa acg cta gaa 158
 Phe Leu Lys Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu
 15 20 25
 tta aaa aaa gat gaa gtg ttt aaa gcg atc atc aaa gac act tca aat 206
 Leu Lys Lys Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn
 30 35 40 45
 gaa caa acc aaa gaa atc acg ctc tat tgg acg cta tat gca aat aaa 254
 Glu Gln Thr Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys
 50 55 60
 ggt tta gtc atc aac atg cgt ttt aac cat ttc cct tac cag ttt att 302
 Gly Leu Val Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile
 65 70 75
 tta tac acc gat cat gcg aga aac acc tat aat ctc aaa gtt ttt gaa 350
 Leu Tyr Thr Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu
 80 85 90
 gaa aaa ttt tct tct aac agc act ctg tcg ctt gtg ttt aaa gat ttt 398
 Glu Lys Phe Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe
 95 100 105
 aaa gaa gat aaa gcc gct tta agg ctt tta gcc ctt atg ccc ctt gtt 446
 Lys Glu Asp Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val
 110 115 120 125
 ttt tct cct aaa gag cct taaggaatgtt gcatgcaaga aaaacaactt 494
 Phe Ser Pro Lys Glu Pro
 130
 aaaaccattc aaaataagat cgcttcc 521

<210> 326
 <211> 131
 <212> PRT
 <213> Helicobacter pylori

<400> 326

<213> Helicobacter pylori

<400> 328

Met	Leu	Ser	Lys	Leu	Pro	Phe	Thr	Gly	Val	Leu	Ala	Leu	Val	Leu	Lys
1				5				10					15		
Ala	Val	His	Val	Ser	Leu	Ala	Glu	Asp	Lys	Ser	Lys	Phe	Thr	Ala	Cys
			20					25					30		
Lys	Asn	Pro	Ala	Ser	Lys	Thr	Asp	Thr	Lys	Thr	Ile	Phe	Phe	Ile	His
		35					40					45			
Tyr	Pro	Leu	Met	Trp	Ser	Tyr	Gln								
	50					55									

<210> 329

<211> 671

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (66)...(611)

<400> 329

aatgacttta	ggggatattc	ttaaagaaaa	actctaaaga	gtgattttta	aagcatgaga	60										
atggc	atg	aga	ttt	aag	ggt	ggt	ggt	gct	ttt	att	tcc	cta	gct	gtc	gct	110
Met	Arg	Phe	Lys	Gly	Val	Val	Ala	Phe	Ile	Ser	Leu	Ala	Val	Ala		
1				5				10					15			
ctt	ggc	ggt	tta	gcc	tat	ttg	ttt	tta	agc	ggt	aaa	aaa	gaa	atg	ccc	158
Leu	Gly	Val	Leu	Ala	Tyr	Leu	Phe	Leu	Ser	Val	Lys	Lys	Glu	Met	Pro	
			20					25					30			
gct	act	tct	cat	gcg	atc	tct	caa	aca	cat	gcg	atc	tct	caa	acc	aat	206
Ala	Thr	Ser	His	Ala	Ile	Ser	Gln	Thr	His	Ala	Ile	Ser	Gln	Thr	Asn	
			35				40					45				
gaa	ggc	ctc	tct	caa	aca	gat	gca	aaa	agc	cat	gac	atc	gat	cta	gaa	254
Glu	Gly	Leu	Ser	Gln	Thr	Asp	Ala	Lys	Ser	His	Asp	Ile	Asp	Leu	Glu	
		50				55					60					
gaa	aat	agc	ccc	act	gaa	acc	tct	cat	aat	gaa	aaa	gcc	tcc	cat	aac	302
Glu	Asn	Ser	Pro	Thr	Glu	Thr	Ser	His	Asn	Glu	Lys	Ala	Ser	His	Asn	
	65				70				75							
gaa	gaa	gat	cac	aat	aac	gcc	ctt	tct	caa	aat	ctt	gat	gcg	caa	gaa	350
Glu	Glu	Asp	His	Asn	Asn	Ala	Leu	Ser	Gln	Asn	Leu	Asp	Ala	Gln	Glu	
	80				85				90					95		
tct	atc	aat	tac	ccc	ggt	gtg	gaa	cat	tat	tct	gaa	atc	cct	ttt	gaa	398
Ser	Ile	Asn	Tyr	Pro	Val	Val	Glu	His	Tyr	Ser	Glu	Ile	Pro	Phe	Glu	
			100					105					110			
gaa	aaa	aaa	agg	gaa	tat	tca	aag	ctt	atc	att	aag	gat	tta	aag	gac	446
Glu	Lys	Lys	Arg	Glu	Tyr	Ser	Lys	Leu	Ile	Ile	Lys	Asp	Leu	Lys	Asp	
			115					120					125			

tat caa tgg tgg tgc tta aaa gaa atc ctc aaa aaa gaa cag att gat 494
Tyr Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp
130 135 140

tac gct tac gat aac acc aaa aac caa cct aac ctc atc atc tat tta 542
Tyr Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu
145 150 155

gat gaa aat aaa aaa gaa cgc ttg ctg gct gat tta gac tat tat aaa 590
Asp Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys
160 165 170 175

ata cgc tat cat gct gtt ttt taaattcaaa ggataaaaat gtatcaagta 641
Ile Arg Tyr His Ala Val Phe
180

gccatttgcg accccatcca tgctaaaggc 671

<210> 330

<211> 182

<212> PRT

<213> Helicobacter pylori

<400> 330

Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala Leu
1 5 10 15
Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro Ala
20 25 30
Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn Glu
35 40 45
Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu Glu
50 55 60
Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn Glu
65 70 75 80
Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser
85 90 95
Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu
100 105 110
Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr
115 120 125
Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr
130 135 140
Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp
145 150 155 160
Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile
165 170 175
Arg Tyr His Ala Val Phe
180

<210> 331

<211> 341

<212> DNA

<213> Helicobacter pylori

<220>
 <221> CDS
 <222> (86)...(295)

<400> 331
 acccacaataa ctaaaaccca ctaacacaat taaccctaac aacacataaa gattgcccac 60
 agacgcgcac aacacgctcg caaca atg gtt gca aaa aca aac aca atc ccc 112
 Met Val Ala Lys Thr Asn Thr Ile Pro
 1 5
 ccc atc gta ggg gta tct ttt tta ttc tgg tgg ctt ggc acg aag cta 160
 Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu
 10 15 20 25
 gaa atg ggc tgg tta gcc ttt tta gcc ttg gcc cat aga atg aat tta 208
 Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu
 30 35 40
 ggc att aaa aaa agc gtg aga aaa aaa gct atg aaa aac cct aac cct 256
 Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro
 45 50 55
 gct cta aaa gtc aaa tac tgg aaa aga ttg ata ttg aaa tagccatata 305
 Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys
 60 65 70
 gtaaagaata gagcataaaa tcccctaataa tcgcca 341

<210> 332
 <211> 70
 <212> PRT
 <213> Helicobacter pylori

<400> 332
 Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe
 1 5 10 15
 Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe
 20 25 30
 Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg
 35 40 45
 Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp
 50 55 60
 Lys Arg Leu Ile Leu Lys
 65 70

<210> 333
 <211> 2481
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (58)...(2430)

<400> 333

tttttttttt tttttgattt ttatttttta aattttttaga ttaaggagag ttgttgg atg 60
Met
1

ttt tta aga gta tac cca aag ctt aga tac gct tta tgt ttc ccc cta 108
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu
5 10 15

ctc gct gag act tgc tat agc gaa gag cgg act tta aat aag gtt acc 156
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr
20 25 30

acc caa gct aaa agg att ttc act tac aac aat gag ttt aaa gta act 204
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr
35 40 45

tct aaa gaa cta gat caa cgc caa agc aat gaa gtc aag gac ttg ttt 252
Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu Phe
50 55 60 65

agg act aac cct gat gtg aat gtg ggc gga ggg agc gtg atg ggg cag 300
Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly Gln
70 75 80

aaa atc tat gtg aga ggc gtt gaa gac agg ctt tta agg gtt aca gtg 348
Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr Val
85 90 95

gat ggg gct gca caa aat ggc aat atc tac cac cac caa ggc aac acc 396
Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn Thr
100 105 110

gtg att gac cct ggc atg ctc aaa agc gtg gaa gtt acc aaa ggc gcg 444
Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly Ala
115 120 125

gcg aat gcg agc gcg ggg cca gga gcg att gcg gga gtg att aaa atg 492
Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys Met
130 135 140 145

gag act aaa gga gcg gct gat ttt atc cct agg ggg aaa aat tat gct 540
Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr Ala
150 155 160

gcc agt ggg gcg gtg agt ttt tat acc aat ttt ggc gat cga gag act 588
Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu Thr
165 170 175

ttc aga tcg gct tat caa aac gcg cat ttt gat att atc gct tac tac 636
Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr Tyr
180 185 190

acg cac caa aac atc ttc tat tat aga agc ggc gct aca gcg atg aaa 684
Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met Lys

195	200	205	
aac ctt ttc aat ccc	aca caa gcc gat aaa	gag cca gga act cct agc	732
Asn Leu Phe Asn Pro Thr	Gln Ala Asp Lys Glu	Pro Gly Thr Pro Ser	
210	215	220 225	
gag caa aac aac gct	ttg att aaa atg aat	ggt tat ttg agc gac aga	780
Glu Gln Asn Asn Ala	Leu Ile Lys Met Asn	Gly Tyr Leu Ser Asp Arg	
230	235	240	
gac acg ctc act ttc	agc tgg aac atg aca	cga gat aac gct aca cgc	828
Asp Thr Leu Thr Phe	Ser Trp Asn Met Thr	Arg Asp Asn Ala Thr Arg	
245	250	255	
cct tta agg agt aac	gct ata ggg tta gcc	tat cct tgt gaa gcc ccc	876
Pro Leu Arg Ser Asn	Ala Ile Gly Leu Ala	Tyr Pro Cys Glu Ala Pro	
260	265	270	
ttt agt cct gat agt	tct caa ggg tgt cct	aat gtg tta gat agt ttc	924
Phe Ser Pro Asp Ser	Ser Gln Gly Cys Pro	Asn Val Leu Asp Ser Phe	
275	280	285	
aca aga tac atg tat	cac tct att aat agt	gcc aac aat ctt tcc tta	972
Thr Arg Tyr Met Tyr	His Ser Ile Asn Ser	Ala Asn Asn Leu Ser Leu	
290	295	300 305	
caa tac aaa agg gaa	gcg gga aat tct ttt	ggc gac cca cga tta gat	1020
Gln Tyr Lys Arg Glu	Ala Gly Asn Ser Phe	Gly Asp Pro Arg Leu Asp	
310	315	320	
ttt acc ctt tat aca	agc atc agg aac gct	cag ttt gat ccc cta ttt	1068
Phe Thr Leu Tyr Thr	Ser Ile Arg Asn Ala	Gln Phe Asp Pro Leu Phe	
325	330	335	
gat cct aat ggc gtt	tat gct aaa ttc ccc	act tct tta gcg agc gca	1116
Asp Pro Asn Gly Val	Tyr Ala Lys Phe Pro	Thr Ser Leu Ala Ser Ala	
340	345	350	
tgg gaa aaa gaa aat	tac cca tgc gtt gaa	ggc gct tat tgc acc cca	1164
Trp Glu Lys Glu Asn	Tyr Pro Cys Val Glu	Gly Ala Tyr Cys Thr Pro	
355	360	365	
agc ttt tca gat gtg	gat aaa cca agc tca	cag cct agg aat ttg ttt	1212
Ser Phe Ser Asp Val	Asp Lys Pro Ser Ser	Gln Pro Arg Asn Leu Phe	
370	375	380 385	
tta aac aac acc ggc	tta aac ctt aaa gtc	gcg cat gtg att gat gaa	1260
Leu Asn Asn Thr Gly	Leu Asn Leu Lys Val	Ala His Val Ile Asp Glu	
390	395	400	
gcc aca gac agc ctt	ttt gaa tac gga ttc	aac tac caa aat ttg agc	1308
Ala Thr Asp Ser Leu	Phe Glu Tyr Gly Phe	Asn Tyr Gln Asn Leu Ser	
405	410	415	
gtt ttt gac gct cgc	atc cct aaa tca gaa	tta tac agg cct aat caa	1356

Val	Phe	Asp	Ala	Arg	Ile	Pro	Lys	Ser	Glu	Leu	Tyr	Arg	Pro	Asn	Gln		
		420					425					430					
gtt	tat	act	gat	gat	aaa	gga	caa	aaa	caa	atc	gct	tgc	tct	ctt	gtg	1404	
Val	Tyr	Thr	Asp	Asp	Lys	Gly	Gln	Lys	Gln	Ile	Ala	Cys	Ser	Leu	Val		
	435					440				445							
aat	aat	aac	ccc	aat	gac	ccc	act	ctg	tgc	caa	aga	ggg	aaa	gcg	aac	1452	
Asn	Asn	Asn	Pro	Asn	Asp	Pro	Thr	Leu	Cys	Gln	Arg	Gly	Lys	Ala	Asn		
450					455					460					465		
ggg	aat	att	tat	gga	ggc	tac	gtg	caa	gcg	aat	tac	tcg	cct	cat	aaa	1500	
Gly	Asn	Ile	Tyr	Gly	Gly	Tyr	Val	Gln	Ala	Asn	Tyr	Ser	Pro	His	Lys		
			470					475						480			
atc	atc	act	ttt	gga	gcc	ggg	gta	agg	tgg	gac	gct	tac	acg	ctt	tat	1548	
Ile	Ile	Thr	Phe	Gly	Ala	Gly	Val	Arg	Trp	Asp	Ala	Tyr	Thr	Leu	Tyr		
			485					490						495			
gat	aaa	gac	tgg	aac	cac	cgc	tac	act	caa	ggc	ttt	agc	cct	agc	gcg	1596	
Asp	Lys	Asp	Trp	Asn	His	Arg	Tyr	Thr	Gln	Gly	Phe	Ser	Pro	Ser	Ala		
	500						505					510					
gct	ctt	gtg	cta	agc	ccc	att	gag	cct	tta	tct	tta	aaa	atc	act	tat	1644	
Ala	Leu	Val	Leu	Ser	Pro	Ile	Glu	Pro	Leu	Ser	Leu	Lys	Ile	Thr	Tyr		
	515					520					525						
tct	caa	gtt	aca	aga	ggg	gtg	atg	cca	gga	gat	ggc	gtg	tac	atg	cgt	1692	
Ser	Gln	Val	Thr	Arg	Gly	Val	Met	Pro	Gly	Asp	Gly	Val	Tyr	Met	Arg		
530					535					540					545		
caa	aac	gat	tta	cga	tac	gcc	aaa	aac	atc	aag	cct	gaa	gtg	ggc	tct	1740	
Gln	Asn	Asp	Leu	Arg	Tyr	Ala	Lys	Asn	Ile	Lys	Pro	Glu	Val	Gly	Ser		
			550						555					560			
aac	gct	gaa	ttt	aat	att	gat	tat	tca	agc	cag	tat	ttt	agc	ggg	agg	1788	
Asn	Ala	Glu	Phe	Asn	Ile	Asp	Tyr	Ser	Ser	Gln	Tyr	Phe	Ser	Gly	Arg		
			565					570						575			
gct	gcg	gcg	ttt	tat	cag	gct	ttg	gat	aat	ttc	atc	tca	caa	tac	gca	1836	
Ala	Ala	Ala	Phe	Tyr	Gln	Ala	Leu	Asp	Asn	Phe	Ile	Ser	Gln	Tyr	Ala		
			580				585					590					
caa	aat	ttg	att	gta	acc	aat	ttg	agt	caa	gcg	att	cgt	att	tat	ggc	1884	
Gln	Asn	Leu	Ile	Val	Thr	Asn	Leu	Ser	Gln	Ala	Ile	Arg	Ile	Tyr	Gly		
	595					600					605						
tat	gaa	gtg	ggt	ggg	act	ttc	aga	tac	aag	ggc	gtg	agt	ttg	aat	gta	1932	
Tyr	Glu	Val	Gly	Gly	Thr	Phe	Arg	Tyr	Lys	Gly	Val	Ser	Leu	Asn	Val		
610					615					620					625		
ggg	gtc	tcg	cgc	acc	tgg	ccc	acc	act	agg	ggg	tat	tta	atg	gcg	gat	1980	
Gly	Val	Ser	Arg	Thr	Trp	Pro	Thr	Thr	Arg	Gly	Tyr	Leu	Met	Ala	Asp		
				630					635					640			

agc tat gag ctt gcc gca agc acc ggt aat gtt ttt atc atc aaa ttg 2028
 Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu
 645 650 655
 gat tac acc atc ccc aaa aca ggg atc aat ctt gca tgg ctt agc cgc 2076
 Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg
 660 665 670
 ttt gtt acc ggt tta gat tat tgc ggg ttt gat att tac ttg cct gat 2124
 Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp
 675 680 685
 tat ggg acg gct gag aaa ccc aaa acc cct acc gat tta gcc aaa tgc 2172
 Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys
 690 695 700 705
 gga tct caa tta ggg tta gtg cat atg cat aaa ccg ggc tat ggc gtg 2220
 Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val
 710 715 720
 agt aat ttt tat atc aat tgg agt cct aaa acc aaa agc cgc tgg aag 2268
 Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp Lys
 725 730 735
 ggt ttg ttg ctt tca gcc gtg ttt aat aat gtt ttc aac aaa ttc tat 2316
 Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr
 740 745 750
 gtg gat caa aca agc cct tat gtc atg agc ccg gat atg cca ggc act 2364
 Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr
 755 760 765
 gac gct gtt aaa aga gcg atc gct gag cct ggg ttt aac gcg cgt ttt 2412
 Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe
 770 775 780 785
 gaa gtg gct tac aaa tgg tagttaatgg agctttaagc gttgcgcatg 2460
 Glu Val Ala Tyr Lys Trp
 790
 cgtgatagca acggctatcg c 2481

<210> 334

<211> 791

<212> PRT

<213> Helicobacter pylori

<400> 334

Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro
 1 5 10 15
 Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val
 20 25 30
 Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val
 35 40 45
 Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu

50						55					60				
Phe	Arg	Thr	Asn	Pro	Asp	Val	Asn	Val	Gly	Gly	Gly	Ser	Val	Met	Gly
65					70					75					80
Gln	Lys	Ile	Tyr	Val	Arg	Gly	Val	Glu	Asp	Arg	Leu	Leu	Arg	Val	Thr
				85					90					95	
Val	Asp	Gly	Ala	Ala	Gln	Asn	Gly	Asn	Ile	Tyr	His	His	Gln	Gly	Asn
			100					105					110		
Thr	Val	Ile	Asp	Pro	Gly	Met	Leu	Lys	Ser	Val	Glu	Val	Thr	Lys	Gly
		115					120					125			
Ala	Ala	Asn	Ala	Ser	Ala	Gly	Pro	Gly	Ala	Ile	Ala	Gly	Val	Ile	Lys
	130					135					140				
Met	Glu	Thr	Lys	Gly	Ala	Ala	Asp	Phe	Ile	Pro	Arg	Gly	Lys	Asn	Tyr
145					150					155					160
Ala	Ala	Ser	Gly	Ala	Val	Ser	Phe	Tyr	Thr	Asn	Phe	Gly	Asp	Arg	Glu
			165						170					175	
Thr	Phe	Arg	Ser	Ala	Tyr	Gln	Asn	Ala	His	Phe	Asp	Ile	Ile	Ala	Tyr
			180					185					190		
Tyr	Thr	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Ser	Gly	Ala	Thr	Ala	Met
		195					200					205			
Lys	Asn	Leu	Phe	Asn	Pro	Thr	Gln	Ala	Asp	Lys	Glu	Pro	Gly	Thr	Pro
	210					215					220				
Ser	Glu	Gln	Asn	Asn	Ala	Leu	Ile	Lys	Met	Asn	Gly	Tyr	Leu	Ser	Asp
225					230					235					240
Arg	Asp	Thr	Leu	Thr	Phe	Ser	Trp	Asn	Met	Thr	Arg	Asp	Asn	Ala	Thr
			245						250					255	
Arg	Pro	Leu	Arg	Ser	Asn	Ala	Ile	Gly	Leu	Ala	Tyr	Pro	Cys	Glu	Ala
			260					265					270		
Pro	Phe	Ser	Pro	Asp	Ser	Ser	Gln	Gly	Cys	Pro	Asn	Val	Leu	Asp	Ser
	275						280					285			
Phe	Thr	Arg	Tyr	Met	Tyr	His	Ser	Ile	Asn	Ser	Ala	Asn	Asn	Leu	Ser
	290					295					300				
Leu	Gln	Tyr	Lys	Arg	Glu	Ala	Gly	Asn	Ser	Phe	Gly	Asp	Pro	Arg	Leu
305					310					315					320
Asp	Phe	Thr	Leu	Tyr	Thr	Ser	Ile	Arg	Asn	Ala	Gln	Phe	Asp	Pro	Leu
			325						330					335	
Phe	Asp	Pro	Asn	Gly	Val	Tyr	Ala	Lys	Phe	Pro	Thr	Ser	Leu	Ala	Ser
			340					345					350		
Ala	Trp	Glu	Lys	Glu	Asn	Tyr	Pro	Cys	Val	Glu	Gly	Ala	Tyr	Cys	Thr
	355					360						365			
Pro	Ser	Phe	Ser	Asp	Val	Asp	Lys	Pro	Ser	Ser	Gln	Pro	Arg	Asn	Leu
	370					375					380				
Phe	Leu	Asn	Asn	Thr	Gly	Leu	Asn	Leu	Lys	Val	Ala	His	Val	Ile	Asp
385					390					395					400
Glu	Ala	Thr	Asp	Ser	Leu	Phe	Glu	Tyr	Gly	Phe	Asn	Tyr	Gln	Asn	Leu
			405						410					415	
Ser	Val	Phe	Asp	Ala	Arg	Ile	Pro	Lys	Ser	Glu	Leu	Tyr	Arg	Pro	Asn
		420						425					430		
Gln	Val	Tyr	Thr	Asp	Asp	Lys	Gly	Gln	Lys	Gln	Ile	Ala	Cys	Ser	Leu
	435						440					445			
Val	Asn	Asn	Asn	Pro	Asn	Asp	Pro	Thr	Leu	Cys	Gln	Arg	Gly	Lys	Ala
	450					455					460				
Asn	Gly	Asn	Ile	Tyr	Gly	Gly	Tyr	Val	Gln	Ala	Asn	Tyr	Ser	Pro	His
465					470					475					480
Lys	Ile	Ile	Thr	Phe	Gly	Ala	Gly	Val	Arg	Trp	Asp	Ala	Tyr	Thr	Leu
			485						490					495	

Tyr	Asp	Lys	Asp	Trp	Asn	His	Arg	Tyr	Thr	Gln	Gly	Phe	Ser	Pro	Ser	
			500					505					510			
Ala	Ala	Leu	Val	Leu	Ser	Pro	Ile	Glu	Pro	Leu	Ser	Leu	Lys	Ile	Thr	
			515					520					525			
Tyr	Ser	Gln	Val	Thr	Arg	Gly	Val	Met	Pro	Gly	Asp	Gly	Val	Tyr	Met	
			530					535					540			
Arg	Gln	Asn	Asp	Leu	Arg	Tyr	Ala	Lys	Asn	Ile	Lys	Pro	Glu	Val	Gly	
																560
Ser	Asn	Ala	Glu	Phe	Asn	Ile	Asp	Tyr	Ser	Ser	Gln	Tyr	Phe	Ser	Gly	
																575
Arg	Ala	Ala	Ala	Phe	Tyr	Gln	Ala	Leu	Asp	Asn	Phe	Ile	Ser	Gln	Tyr	
																590
Ala	Gln	Asn	Leu	Ile	Val	Thr	Asn	Leu	Ser	Gln	Ala	Ile	Arg	Ile	Tyr	
																605
Gly	Tyr	Glu	Val	Gly	Gly	Thr	Phe	Arg	Tyr	Lys	Gly	Val	Ser	Leu	Asn	
																620
Val	Gly	Val	Ser	Arg	Thr	Trp	Pro	Thr	Thr	Arg	Gly	Tyr	Leu	Met	Ala	
																640
Asp	Ser	Tyr	Glu	Leu	Ala	Ala	Ser	Thr	Gly	Asn	Val	Phe	Ile	Ile	Lys	
																655
Leu	Asp	Tyr	Thr	Ile	Pro	Lys	Thr	Gly	Ile	Asn	Leu	Ala	Trp	Leu	Ser	
																670
Arg	Phe	Val	Thr	Gly	Leu	Asp	Tyr	Cys	Gly	Phe	Asp	Ile	Tyr	Leu	Pro	
																685
Asp	Tyr	Gly	Thr	Ala	Glu	Lys	Pro	Lys	Thr	Pro	Thr	Asp	Leu	Ala	Lys	
																700
Cys	Gly	Ser	Gln	Leu	Gly	Leu	Val	His	Met	His	Lys	Pro	Gly	Tyr	Gly	
																720
Val	Ser	Asn	Phe	Tyr	Ile	Asn	Trp	Ser	Pro	Lys	Thr	Lys	Ser	Arg	Trp	
																735
Lys	Gly	Leu	Leu	Ser	Ala	Val	Phe	Asn	Asn	Val	Phe	Asn	Lys	Phe		
																750
Tyr	Val	Asp	Gln	Thr	Ser	Pro	Tyr	Val	Met	Ser	Pro	Asp	Met	Pro	Gly	
																765
Thr	Asp	Ala	Val	Lys	Arg	Ala	Ile	Ala	Glu	Pro	Gly	Phe	Asn	Ala	Arg	
																780
Phe	Glu	Val	Ala	Tyr	Lys	Trp										
																790

<210> 335
 <211> 477
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (120)...(428)

<400> 335
 gtcggtcggg taatgttcaa attcacaaat gagtctgaag acaaagaagt cttgatctag 60
 aagccgaaat ttcataccg cacttagaat tgcgtcaaaa acaaattgat gcgctgttg 119
 gtg cac gat att acc aag cta tgt tac acc aaa cca cta ggg tgt gtt 167
 Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val
 1 5 10 15

gtg ctg ttc agc aag gat act gat ctt gtg cct gtg tta gaa tcc gct	215
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala	
20 25 30	
tgg gag aaa ggc ttt gaa gtc ttc att gct aac att caa gaa tgc ccc	263
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro	
35 40 45	
aat tct gtc cct tca gac ttg aag aag tct tgc aat gtg agg gaa cgc	311
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg	
50 55 60	
agt gtc gct gaa att gta gat aac ttg ccc aaa aat cag cac act ccc	359
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro	
65 70 75 80	
aag aaa aag aac ttt tcc acc aac gag cct ttt aac aac cca ttt aaa	407
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys	
85 90 95	
gac caa ctc ttt aag aag aac taacacgatc cccacaccaa ggggacaaaa	458
Asp Gln Leu Phe Lys Lys Asn	
100	

aagcacccat tttaaaagg 477

<210> 336
 <211> 103
 <212> PRT
 <213> Helicobacter pylori

<400> 336

Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val	
1 5 10 15	
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala	
20 25 30	
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro	
35 40 45	
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg	
50 55 60	
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro	
65 70 75 80	
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys	
85 90 95	
Asp Gln Leu Phe Lys Lys Asn	
100	

<210> 337
 <211> 685
 <212> DNA
 <213> Helicobacter pylori

<220>

<221> CDS
 <222> (220)...(624)

<221> misc_feature
 <222> 121
 <223> n = A,T,C or G

<400> 337
 tcttttgaaa ttgcctgatg tggaaaaaga aatgccc aaa gagacgactc aaaaaagctt 60
 gttttcgcac aaacactttg tttttggggc ttggggatct ttttttatgt ggggggagaa 120
 ntggcgattg gctcattctt ggtgctaagc tttgaaaagc ttttgaattt agactctcaa 180
 tcaagcgcgc attacttggg gtattattgg ggagcgcg atg gtg ggc cgt ttc 234
 Met Val Gly Arg Phe
 1 5

tta ggc agt gtg ttg atg aat aaa att gcc cct aat aaa tac ttg gct 282
 Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala
 10 15 20

ttc aac gcc tta agc tct att gtt ctc atc gct tta gcc att atc att 330
 Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile
 25 30 35

gga ggc aag atc gct tta ttc gct ctg act ttt gtg ggc ttt ttc aac 378
 Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn
 40 45 50

tct atc atg ttc cct acc atc ttt tct ttg gct acg ctc aat tta ggg 426
 Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly
 55 60 65

cat ctc act tct aaa gct tct ggg gtg att agc atg gcg att gtg gga 474
 His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly
 70 75 80 85

ggg gcg tta atc ccc ccc att caa ggt gcg gtt aca gac atg cta aca 522
 Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr
 90 95 100

gca acc gaa tca aat ttg ctc tac gct tat ggt gtg ccg ttg ttg tgc 570
 Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys
 105 110 115

tat ttt tat att ctc ttc ttt gcg ctt aaa ggg tat aag caa gaa gaa 618
 Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu
 120 125 130

aac tcc taataaaagg gggggtttct ttcttctttc ctttctttta tcttgtttta 674
 Asn Ser
 135

aaaatcagta a 685

<210> 338
 <211> 135

<212> PRT
 <213> Helicobacter pylori

<400> 338
 Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro
 1 5 10 15
 Asn Lys Tyr Leu Ala Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala
 20 25 30
 Leu Ala Ile Ile Ile Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe
 35 40 45
 Val Gly Phe Phe Asn Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala
 50 55 60
 Thr Leu Asn Leu Gly His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser
 65 70 75 80
 Met Ala Ile Val Gly Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val
 85 90 95
 Thr Asp Met Leu Thr Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly
 100 105 110
 Val Pro Leu Leu Cys Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly
 115 120 125
 Tyr Lys Gln Glu Glu Asn Ser
 130 135

<210> 339
 <211> 809
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (58)...(765)

<400> 339
 accgatcact aaaaccaatg taacttaccg ctcttttacag cgtaagtgag aaaagga atg 60
 Met
 1
 cat ttg aat acg gat ttt agc cat atc acc gat ata gag ggc atg cgt 108
 His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met Arg
 5 10 15
 ttt atc aat gaa gaa gac gct ttg aac aaa ttg att aat gaa atc cac 156
 Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile His
 20 25 30
 acg cgc cac att gat tta aaa gat tcc atc atg ctc gct ttg agt ttt 204
 Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser Phe
 35 40 45
 aac gct ctg tat tta gct cac gct tta gcg caa aaa ttt gga gcg act 252
 Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala Thr
 50 55 60 65
 tat gat ata ctt ttt tta gaa cct atc cta gcc cct tta aac tca aaa 300

Tyr	Asp	Ile	Leu	Phe	Leu	Glu	Pro	Ile	Leu	Ala	Pro	Leu	Asn	Ser	Lys		
				70					75					80			
tgc	gag	atc	gct	tta	gtg	agt	gag	agc	atg	gat	ata	gtg	atg	aat	gaa	348	
Cys	Glu	Ile	Ala	Leu	Val	Ser	Glu	Ser	Met	Asp	Ile	Val	Met	Asn	Glu		
			85					90					95				
agt	ttg	atc	aat	tcc	ttt	gac	atc	act	tta	gac	tat	gtt	tat	ggg	gaa	396	
Ser	Leu	Ile	Asn	Ser	Phe	Asp	Ile	Thr	Leu	Asp	Tyr	Val	Tyr	Gly	Glu		
		100					105					110					
gcc	aag	cga	gct	tat	gaa	gaa	gac	att	ttg	tct	cac	atc	tat	cag	tat	444	
Ala	Lys	Arg	Ala	Tyr	Glu	Glu	Asp	Ile	Leu	Ser	His	Ile	Tyr	Gln	Tyr		
	115					120					125						
cgc	aaa	ggc	aat	gcg	atc	aaa	agc	tta	aaa	gat	aaa	aat	att	ttt	atc	492	
Arg	Lys	Gly	Asn	Ala	Ile	Lys	Ser	Leu	Lys	Asp	Lys	Asn	Ile	Phe	Ile		
	130				135					140					145		
gta	gat	agg	ggg	att	gaa	acc	ggg	ttt	aga	gca	ggg	tta	ggc	gtg	caa	540	
Val	Asp	Arg	Gly	Ile	Glu	Thr	Gly	Phe	Arg	Ala	Gly	Leu	Gly	Val	Gln		
				150					155					160			
act	tgc	ttg	aaa	aaa	gaa	tgc	caa	gac	att	tat	att	tta	acc	ccc	att	588	
Thr	Cys	Leu	Lys	Lys	Glu	Cys	Gln	Asp	Ile	Tyr	Ile	Leu	Thr	Pro	Ile		
			165					170					175				
gtc	gcg	caa	aat	gtc	gct	caa	ggc	tta	gaa	agt	ttg	tgc	gat	ggg	gtg	636	
Val	Ala	Gln	Asn	Val	Ala	Gln	Gly	Leu	Glu	Ser	Leu	Cys	Asp	Gly	Val		
		180					185					190					
att	agt	gtg	tat	cgc	cct	gaa	tgt	ttt	gtc	tct	gtg	gag	cat	cat	tat	684	
Ile	Ser	Val	Tyr	Arg	Pro	Glu	Cys	Phe	Val	Ser	Val	Glu	His	His	Tyr		
		195				200					205						
aaa	gaa	ctc	aag	cga	tta	agc	aat	gaa	gaa	gtt	gaa	aaa	tac	ttg	ggc	732	
Lys	Glu	Leu	Lys	Arg	Leu	Ser	Asn	Glu	Glu	Val	Glu	Lys	Tyr	Leu	Gly		
	210				215					220					225		
gct	aac	aac	atg	cct	aat	tta	aaa	aag	gaa	cat	taa	aat	atg	gga	ttttatcacc	785	
Ala	Asn	Asn	Met	Pro	Asn	Leu	Lys	Lys	Glu	His							
				230					235								
atcaattcta gtaacaaaac cgaa																809	
<210> 340																	
<211> 236																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 340																	
Met	His	Leu	Asn	Thr	Asp	Phe	Ser	His	Ile	Thr	Asp	Ile	Glu	Gly	Met		
1				5					10					15			
Arg	Phe	Ile	Asn	Glu	Glu	Asp	Ala	Leu	Asn	Lys	Leu	Ile	Asn	Glu	Ile		
			20					25					30				

His	Thr	Arg	His	Ile	Asp	Leu	Lys	Asp	Ser	Ile	Met	Leu	Ala	Leu	Ser
		35					40					45			
Phe	Asn	Ala	Leu	Tyr	Leu	Ala	His	Ala	Leu	Ala	Gln	Lys	Phe	Gly	Ala
	50					55					60				
Thr	Tyr	Asp	Ile	Leu	Phe	Leu	Glu	Pro	Ile	Leu	Ala	Pro	Leu	Asn	Ser
65					70					75				80	
Lys	Cys	Glu	Ile	Ala	Leu	Val	Ser	Glu	Ser	Met	Asp	Ile	Val	Met	Asn
				85					90					95	
Glu	Ser	Leu	Ile	Asn	Ser	Phe	Asp	Ile	Thr	Leu	Asp	Tyr	Val	Tyr	Gly
			100					105					110		
Glu	Ala	Lys	Arg	Ala	Tyr	Glu	Glu	Asp	Ile	Leu	Ser	His	Ile	Tyr	Gln
		115						120				125			
Tyr	Arg	Lys	Gly	Asn	Ala	Ile	Lys	Ser	Leu	Lys	Asp	Lys	Asn	Ile	Phe
	130					135					140				
Ile	Val	Asp	Arg	Gly	Ile	Glu	Thr	Gly	Phe	Arg	Ala	Gly	Leu	Gly	Val
145					150					155					160
Gln	Thr	Cys	Leu	Lys	Lys	Glu	Cys	Gln	Asp	Ile	Tyr	Ile	Leu	Thr	Pro
				165					170						175
Ile	Val	Ala	Gln	Asn	Val	Ala	Gln	Gly	Leu	Glu	Ser	Leu	Cys	Asp	Gly
			180					185					190		
Val	Ile	Ser	Val	Tyr	Arg	Pro	Glu	Cys	Phe	Val	Ser	Val	Glu	His	His
		195					200					205			
Tyr	Lys	Glu	Leu	Lys	Arg	Leu	Ser	Asn	Glu	Glu	Val	Glu	Lys	Tyr	Leu
	210					215					220				
Gly	Ala	Asn	Asn	Met	Pro	Asn	Leu	Lys	Lys	Glu	His				
225					230					235					

<210> 341

<211> 325

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (70)...(285)

<400> 341

taacacaagc caccatgagc atactatcgc catagttggc aataaagcag tgattcttac 60
ggagcgtta atg gca aga gat gat gtt ata gaa gtg gat ggg aaa gtg att 111

Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile
1 5 10

gag gcg ttg cct aac gct act ttt aag gtg gag tta gac aat aag cat 159
Glu Ala Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His
15 20 25 30

gtg gtg ttg tgc cgt att tct gga aag atg cgc atg cac tat att agg 207
Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg
35 40 45

att gct tta ggc gat agg gtt aag cta gag ctt acg ccc tat agc tta 255
Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu
50 55 60

gac aaa ggt cgg ata act ttt aga tat aaa tgaattttaag gggtattttca 305
 Asp Lys Gly Arg Ile Thr Phe Arg Tyr Lys
 65 70

atgaaaatat gttaatatataa 325

<210> 342
 <211> 72
 <212> PRT
 <213> Helicobacter pylori

<400> 342
 Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile Glu Ala
 1 5 10 15
 Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His Val Val
 20 25 30
 Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg Ile Ala
 35 40 45
 Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu Asp Lys
 50 55 60
 Gly Arg Ile Thr Phe Arg Tyr Lys
 65 70

<210> 343
 <211> 360
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (52)...(309)

<400> 343
 atcgctcaaa tttcaacgac catgcttggt aaaaaaaact aaaggaatgt t atg caa 57
 Met Gln
 1

gat gaa tta ttt gaa acc gaa aaa atc ccc cca aaa aac act aaa aat 105
 Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr Lys Asn
 5 10 15

act aaa aac gcc cct aaa aaa agt ttt gaa gag cat gtt cat tcc cta 153
 Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His Ser Leu
 20 25 30

gag cga gcc ata gat cgc ttg aat gat ccc aat tta tcc tta aaa gac 201
 Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu Lys Asp
 35 40 45 50

ggg atg gat ttg tat aaa acg gcc atg caa gag ttg ttt ttg gct caa 249
 Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu Ala Gln
 55 60 65

aag ctt tta gaa aac gct tat tta gag cat gaa aaa ctc caa acg cca 297

ttt tgg aat tgc gcg att aaa aag ggc tat tct ggg gtg gta act ttc	249
Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe	
55 60 65	
act aaa aaa gag cct tta agc gtg agc tat ggt att aat atg gaa gag	297
Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu	
70 75 80	
cat gac aaa gaa ggg cgc gta ata act tgc gaa ttt gag tcg ttt tat	345
His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr	
85 90 95 100	
ttg gtg aat gtt tat acc cct aat tcc caa caa gcc cta tcc agg ctt	393
Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu	
105 110 115	
agt tat cgc atg agt tgg gaa gtg gag ttt aag aaa ttt tta aaa gct	441
Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala	
120 125 130	
tta gag ttg aaa aaa ccg gtc att gtg tgt ggg gat ttg aat gtg gct	489
Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala	
135 140 145	
cac aat gaa att gat tta gaa aac ccc aaa acc aac cga aaa aat gcc	537
His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala	
150 155 160	
ggc ttt agc gat gaa gag aga gaa aaa ttc agc gag ctt ttg aac gcc	585
Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala	
165 170 175 180	
ggg ttt att gac act ttc cgt tat ttt tac cct aac aaa gaa aag gct	633
Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala	
185 190 195	
tac acc tgg tgg agt tac atg caa caa gca agg gat aaa aac att ggt	681
Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly	
200 205 210	
tgg cgc att gat tat ttt tta tgc tct aac cct tta aaa acg cgc tta	729
Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu	
215 220 225	
aaa gac gct tta atc tat aaa gat att tta ggg agc gat cat tgc ccg	777
Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro	
230 235 240	
gta ggg ttg gaa tta gtt taaaggtaga aagtgtgcga aataaagaca	825
Val Gly Leu Glu Leu Val	
245 250	
gaaaaaagcc ttacaa	841
<210> 346	

<211> 250
 <212> PRT
 <213> Helicobacter pylori

<400> 346
 Met Lys Leu Ile Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr
 1 5 10 15
 Lys Gly Phe Met Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys
 20 25 30
 Ile Gln Glu Ser Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys
 35 40 45
 Gly Tyr Phe Asp Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly
 50 55 60
 Val Val Thr Phe Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile
 65 70 75 80
 Asn Met Glu Glu His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe
 85 90 95
 Glu Ser Phe Tyr Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala
 100 105 110
 Leu Ser Arg Leu Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys
 115 120 125
 Phe Leu Lys Ala Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp
 130 135 140
 Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn
 145 150 155 160
 Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu
 165 170 175
 Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn
 180 185 190
 Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp
 195 200 205
 Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu
 210 215 220
 Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser
 225 230 235 240
 Asp His Cys Pro Val Gly Leu Glu Leu Val
 245 250

<210> 347
 <211> 618
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (62)...(571)

<400> 347
 agaatgcgag cgtaaataaa gaaatttatg tgcctaataa gcttggttaat tttgttatcg 60
 c atg agg gct tta ctt ttt ttt att ttg tta ctt tgg ttc aag ggt tgt 109
 Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys
 1 5 10 15
 ggg tat aag cct att gca gct tac gct caa aac gct tta ggc gat agc 157

Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser
 20 25 30
 gta tac gtg aaa ctc att gtg aat ttg cct aac cct gaa aac tct gta 205
 Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val
 35 40 45
 gag ttt aag gat ttg atg aat cgt tta gtc gtg caa cgc ttc caa agc 253
 Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser
 50 55 60
 cgc tta gcg agt gaa aag gat gcg gat tct atc att att ata gaa atc 301
 Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile
 65 70 75 80
 acg aat gta acc gat acg agt atc acg caa aat aaa gaa ggc ttc acg 349
 Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr
 85 90 95
 act ttc tat cgc gca acc gtg tct gtg aat tac acc tac gat aat aaa 397
 Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys
 100 105 110
 aga ggc aca caa aag act ttt caa gat agc ggg tat tac aat tac gct 445
 Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala
 115 120 125
 gtg aat ttg caa gac ccc ctt aat acc tac cag aac cgc tat tat gct 493
 Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala
 130 135 140
 atc aat cag gct gtg gaa cag act ttg act aaa ttt gtg gct caa atc 541
 Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile
 145 150 155 160
 gct tat gag ggg aaa ttc aat aat gaa aaa tagccctttg aatggattga 591
 Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys
 165 170
 atggactaaa ggcgttttta gaaacaa 618

<210> 348

<211> 170

<212> PRT

<213> *Helicobacter pylori*

<400> 348

Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys
 1 5 10 15
 Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser
 20 25 30
 Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val
 35 40 45
 Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser
 50 55 60

Arg	Leu	Ala	Ser	Glu	Lys	Asp	Ala	Asp	Ser	Ile	Ile	Ile	Ile	Glu	Ile
65					70					75				80	
Thr	Asn	Val	Thr	Asp	Thr	Ser	Ile	Thr	Gln	Asn	Lys	Glu	Gly	Phe	Thr
				85					90					95	
Thr	Phe	Tyr	Arg	Ala	Thr	Val	Ser	Val	Asn	Tyr	Thr	Tyr	Asp	Asn	Lys
			100					105					110		
Arg	Gly	Thr	Gln	Lys	Thr	Phe	Gln	Asp	Ser	Gly	Tyr	Tyr	Asn	Tyr	Ala
		115					120					125			
Val	Asn	Leu	Gln	Asp	Pro	Leu	Asn	Thr	Tyr	Gln	Asn	Arg	Tyr	Tyr	Ala
	130					135					140				
Ile	Asn	Gln	Ala	Val	Glu	Gln	Thr	Leu	Thr	Lys	Phe	Val	Ala	Gln	Ile
145					150					155					160
Ala	Tyr	Glu	Gly	Lys	Phe	Asn	Asn	Glu	Lys						
				165					170						

<210> 349
 <211> 1277
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (61)...(1224)

<400> 349
 aatacccata aaatacctta agagaacgcc tattcaaaaa ccaaaaataa ggaaatccta 60
 atg act aca gac aga aat ttg ttt ttt tgc gct tcg cta ttg att ttt 108
 Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
 1 5 10 15

ttg ggg gta ttg atg agc tat tcg ctc tca act tac acc aca gtg gtg 156
 Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
 20 25 30

ctg tat cat tat ggg gag ttc cat ttt ttc ata cgc cag ctt gtg agc 204
 Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
 35 40 45

gcg atc ata ggg att gtt atc atg tgg ggg ttg tct agg gtt gat cct 252
 Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
 50 55 60

agc aag tgg ttt agc cgt ttg ggg ttt ttt ctt ctt ttt gtc cca cca 300
 Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro
 65 70 75 80

tta ctc att att ggc atg ttt ttt ttg cca gaa agc ctt tct agc agt 348
 Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser
 85 90 95

gct ggg ggg gcg aag cga tgg att cgt ttg ggg ttt ttt tct cta gcg 396
 Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala
 100 105 110

cct ttg gag ttt ttg aag att ggt ttc acc ttt ttt ctt gcg tgg agt	444
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser	
115 120 125	
ttg tct cgc act ttt gtg gca aaa gaa aag gct aat gtt aaa gaa gaa	492
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu	
130 135 140	
ctc atc act ttt gtg cct tat tca gtg gtg ttt gta gcc tta gcg att	540
Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile	
145 150 155 160	
ggg gtg ggg gtt ttg caa aac gat ttg ggg cag att gtt ctt ttg ggg	588
Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly	
165 170 175	
gcg gtt tta gcg gtg ttg ttg gtt ttt tct ggg ggg agc gtg cat ttg	636
Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu	
180 185 190	
ttt ggc ttg att att tca ggg gcg ttt gcg atc agc gtt tta gcg att	684
Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile	
195 200 205	
gtt aca agc gag cat agg att ttg cgc ctg aaa ttg tgg tgg tct aat	732
Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn	
210 215 220	
ttg caa aat tcg ctt ttc acg ctc ttg ccg gat aga tta gcg aac gct	780
Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala	
225 230 235 240	
ctt aga ata agc gac ttg ccc gaa tcc tat cag gtc ttt cat gca ggc	828
Leu Arg Ile Ser Asp Leu Pro Glu Ser Tyr Gln Val Phe His Ala Gly	
245 250 255	
aat gcc atg cat aat ggg ggg ttg ttt ggg caa ggg ctt ggg ctt ggg	876
Asn Ala Met His Asn Gly Gly Leu Phe Gly Gln Gly Leu Gly Leu Gly	
260 265 270	
caa atc aag ctt ggg ttt ttg agc gaa gtg cat acg gac atg gtc tta	924
Gln Ile Lys Leu Gly Phe Leu Ser Glu Val His Thr Asp Met Val Leu	
275 280 285	
gct ggg atc gcc gaa gaa tgg ggg ttt ttg ggg cta tgc gtt tgt ttt	972
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe	
290 295 300	
att ttg ttt tct gtt ttg att gtt ttg att ttt agg atc gct aac cgc	1020
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg	
305 310 315 320	
ttg aaa gag cca aaa tat tcg cta ttt tgc gtg ggc gtg gtg ctg ctt	1068
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu	
325 330 335	

att agt ttt tct ttg gtg atc aac gcc ttt ggg gtg ggc ggg att ctt 1116
 Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu
 340 345 350

ccg gtt aaa ggt cta gcg gtg ccg ttt ttg agc tat gga ggg agt tcg 1164
 Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser
 355 360 365

ctt cta gcg aat tgt atc gct ata ggg ctt gtt cta agc cta gcg cga 1212
 Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg
 370 375 380

tac acg aaa ggc taaaaacatc aaccctttt taaaaattaa tgccataaaa 1264
 Tyr Thr Lys Gly
 385

agggctcaac ctc 1277

<210> 350
 <211> 388
 <212> PRT
 <213> Helicobacter pylori

<400> 350
 Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
 1 5 10 15
 Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
 20 25 30
 Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
 35 40 45
 Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
 50 55 60
 Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro
 65 70 75 80
 Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser
 85 90 95
 Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala
 100 105 110
 Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser
 115 120 125
 Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu
 130 135 140
 Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile
 145 150 155 160
 Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly
 165 170 175
 Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu
 180 185 190
 Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile
 195 200 205
 Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn
 210 215 220
 Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala
 225 230 235 240

ttc ttt aag ggg agt ttg gaa agt tgt gtg gat caa aag att tgt tat	344
Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile Cys Tyr	
85 90 95	
tat gag cat aaa gat ggc aag gtt tct ttt gtg gtg aat gac agg gag	392
Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp Arg Glu	
100 105 110	
aag ttt tat aaa cat gtg ctt aaa gac tta ggg aca gag ctt tcg ctc	440
Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu Ser Leu	
115 120 125 130	
cct ttg ttt aac tgg ctt tac aaa ggc tcg gat ttt ggg gct ttg cat	488
Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala Leu His	
135 140 145	
gag cag ttt ggg gat atg tat gat ggg tat atc aaa tac ttg atc agt	536
Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu Ile Ser	
150 155 160	
atg gtt aga ata agc caa aaa gaa aag gct aga aaa gtg gat gca atc	584
Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp Ala Ile	
165 170 175	
gtt ctt aag aaa atg gaa gaa caa gct gag aaa gac act aag gca gcg	632
Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys Ala Ala	
180 185 190	
ttt caa aag agg agc agt ggg gag ctt gaa agc cat act gat agc cct	680
Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp Ser Pro	
195 200 205 210	
gaa ttt ata agc tct tct aag agg aca cag aac gct tct aat tcg gat	728
Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn Ser Asp	
215 220 225	
ctc aat tct atg acc aat gct aac gcg ctc aaa gaa aca gct tca aaa	776
Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala Ser Lys	
230 235 240	
gag cca gag gct tct tca aaa aaa gag aaa aag tct aag aaa aaa cgt	824
Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys Lys Arg	
245 250 255	
cgc ctt tca aag aaa gaa aaa caa caa caa gcc ttg caa caa gag ttt	872
Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln Glu Phe	
260 265 270	
gaa aaa caa att agc gac tct agt aag tct gaa aaa tagtaataat	918
Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys	
275 280 285	
agttaagctt accttttttag ggggctttca ataaatctct taa	961

<210> 352
 <211> 286
 <212> PRT
 <213> Helicobacter pylori

<400> 352
 Val Lys Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg
 1 5 10 15
 Ala Glu Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val
 20 25 30
 Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg
 35 40 45
 Val Leu Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe
 50 55 60
 Asn Arg Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe
 65 70 75 80
 Gly Ala Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile
 85 90 95
 Cys Tyr Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp
 100 105 110
 Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu
 115 120 125
 Ser Leu Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala
 130 135 140
 Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu
 145 150 155 160
 Ile Ser Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp
 165 170 175
 Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys
 180 185 190
 Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp
 195 200 205
 Ser Pro Glu Phe Ile Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn
 210 215 220
 Ser Asp Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala
 225 230 235 240
 Ser Lys Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys
 245 250 255
 Lys Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln
 260 265 270
 Glu Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
 275 280 285

<210> 353
 <211> 1555
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(1499)

<400> 353
 ctttttagcc tcaagacttg ggctttaaca ttaaagaatt attttaagga atg atc 56

															Met	Ile	
															1		
atg gaa aaa tac cat agc gac caa gaa tac gaa gaa atc atc acc gac	104																
Met Glu Lys Tyr His Ser Asp Gln Glu Tyr Glu Glu Ile Ile Thr Asp																	
		5					10					15					
caa tta ggc gat atg caa tta agg gaa aat ttg cgt tct gca atg gat	152																
Gln Leu Gly Asp Met Gln Leu Arg Glu Asn Leu Arg Ser Ala Met Asp																	
		20					25				30						
acc tta agg gct aat cgt aag aat ctc ctt aaa aat cgt tac agc gaa	200																
Thr Leu Arg Ala Asn Arg Lys Asn Leu Leu Lys Asn Arg Tyr Ser Glu																	
		35				40				45					50		
tgg gaa aat tta agg gaa tta ggc aaa gaa gtc aag ctt aaa atc tta	248																
Trp Glu Asn Leu Arg Glu Leu Gly Lys Glu Val Lys Leu Lys Ile Leu																	
				55					60						65		
tcc agg ctt gat gaa tat ttg gaa ttg ttt gaa aaa aac gcc act caa	296																
Ser Arg Leu Asp Glu Tyr Leu Glu Leu Phe Glu Lys Asn Ala Thr Gln																	
				70				75					80				
aac ggc ttt aaa atc cat tac gct aaa gac ggc gat gaa gct aat gaa	344																
Asn Gly Phe Lys Ile His Tyr Ala Lys Asp Gly Asp Glu Ala Asn Glu																	
			85				90					95					
atc att tac aac ctc gct aaa gaa aag aat atc aag cgc att tta aag	392																
Ile Ile Tyr Asn Leu Ala Lys Glu Lys Asn Ile Lys Arg Ile Leu Lys																	
		100					105				110						
caa aaa tcc atg gcg agc gaa gaa att ggc ttg aac cat tac ttg aaa	440																
Gln Lys Ser Met Ala Ser Glu Glu Ile Gly Leu Asn His Tyr Leu Lys																	
		115				120				125					130		
gaa aag ggc att caa gca caa gaa acg gat ttg ggc gaa ttg att atc	488																
Glu Lys Gly Ile Gln Ala Gln Glu Thr Asp Leu Gly Glu Leu Ile Ile																	
				135				140						145			
caa ctc atc aat gaa cac cct gtg cat att gtc gtg cca gct atc cat	536																
Gln Leu Ile Asn Glu His Pro Val His Ile Val Val Pro Ala Ile His																	
				150				155						160			
aaa aac cgc aag caa atc ggt aag att ttt gaa gaa aaa ctc aac gcc	584																
Lys Asn Arg Lys Gln Ile Gly Lys Ile Phe Glu Glu Lys Leu Asn Ala																	
			165				170					175					
gct tat gaa gaa gag cct gaa aag ctt aat gcg atc gcc aga aaa cac	632																
Ala Tyr Glu Glu Glu Pro Glu Lys Leu Asn Ala Ile Ala Arg Lys His																	
		180				185				190							
atg cgc aaa gaa ttt gaa agc ttt aaa atg ggg att agt ggg gtt aat	680																
Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly Val Asn																	
		195				200				205					210		

ttt gct atc gct aac gaa gga gcg atc tgg tta gtg gaa aat gaa ggc	728
Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn Glu Gly	
215 220 225	
aat ggc aga atg agc acc act gca tgc gat gtg cat gtc gca att tgt	776
Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala Ile Cys	
230 235 240	
ggg att gaa aaa tta gta gaa agc ttt gat gat gcg gcg att tta aac	824
Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile Leu Asn	
245 250 255	
aat ttg ctc gcc cca agc gct gtg ggt gtg cct atc act tgc tat caa	872
Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys Tyr Gln	
260 265 270	
aac att atc aca ggc cct aga aaa gag ggc gat tta gac ggc cct aaa	920
Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly Pro Lys	
275 280 285 290	
gaa gcc cac atc att tta tta gac aac aac cgc tct aat att ttg gct	968
Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile Leu Ala	
295 300 305	
gat gaa aag tat tat cgc gct ctt tca tgc atc cgt tgc ggg act tgt	1016
Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly Thr Cys	
310 315 320	
ttg aac cac tgc cct gtg tat gat aaa atc ggt ggg cat gcc tat ctt	1064
Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala Tyr Leu	
325 330 335	
tct act tat cct ggc cct ata ggc gtg gtg gta tcc ccc caa ctc ttt	1112
Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln Leu Phe	
340 345 350	
ggc ttg aat aat tac ggg cat atc cct aat ttg tgc agt ctt tgc ggg	1160
Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu Cys Gly	
355 360 365 370	
cgt tgc act gaa gta tgc ccc gta gaa atc cct tta gcc gaa ctc att	1208
Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu Leu Ile	
375 380 385	
agg gat tta cga tcc gat aaa gtg ggc gag ggc agg ggt gta att aag	1256
Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val Ile Lys	
390 395 400	
ggg gct aaa agc acc caa cac agc ggg atg gaa aaa ttc tct atg aaa	1304
Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser Met Lys	
405 410 415	
atg ttt gcc aaa atg gca agc gat ggg gct aag tgg cgt ttc caa ttg	1352
Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe Gln Leu	
420 425 430	

aaa atg gct caa ttt ttc tcg cct tta ggc aag ctt tta gct ccc ata 1400
Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala Pro Ile
435 440 445 450

Ile	Cys	Gly	Ile	Glu	Lys	Leu	Val	Glu	Ser	Phe	Asp	Asp	Ala	Ala	Ile	
				245					250					255		
Leu	Asn	Asn	Leu	Leu	Ala	Pro	Ser	Ala	Val	Gly	Val	Pro	Ile	Thr	Cys	
			260					265					270			
Tyr	Gln	Asn	Ile	Ile	Thr	Gly	Pro	Arg	Lys	Glu	Gly	Asp	Leu	Asp	Gly	
		275					280					285				
Pro	Lys	Glu	Ala	His	Ile	Ile	Leu	Leu	Asp	Asn	Asn	Arg	Ser	Asn	Ile	
	290					295					300					
Leu	Ala	Asp	Glu	Lys	Tyr	Tyr	Arg	Ala	Leu	Ser	Cys	Ile	Arg	Cys	Gly	
305					310					315					320	
Thr	Cys	Leu	Asn	His	Cys	Pro	Val	Tyr	Asp	Lys	Ile	Gly	Gly	His	Ala	
			325						330					335		
Tyr	Leu	Ser	Thr	Tyr	Pro	Gly	Pro	Ile	Gly	Val	Val	Val	Ser	Pro	Gln	
		340					345						350			
Leu	Phe	Gly	Leu	Asn	Asn	Tyr	Gly	His	Ile	Pro	Asn	Leu	Cys	Ser	Leu	
	355					360					365					
Cys	Gly	Arg	Cys	Thr	Glu	Val	Cys	Pro	Val	Glu	Ile	Pro	Leu	Ala	Glu	
	370					375				380						
Leu	Ile	Arg	Asp	Leu	Arg	Ser	Asp	Lys	Val	Gly	Glu	Gly	Arg	Gly	Val	
385					390				395						400	
Ile	Lys	Gly	Ala	Lys	Ser	Thr	Gln	His	Ser	Gly	Met	Glu	Lys	Phe	Ser	
			405					410					415			
Met	Lys	Met	Phe	Ala	Lys	Met	Ala	Ser	Asp	Gly	Ala	Lys	Trp	Arg	Phe	
		420					425					430				
Gln	Leu	Lys	Met	Ala	Gln	Phe	Phe	Ser	Pro	Leu	Gly	Lys	Leu	Leu	Ala	
	435					440					445					
Pro	Ile	Leu	Pro	Leu	Val	Lys	Glu	Trp	Ala	Ser	Val	Arg	Thr	Leu	Pro	
	450				455					460						
Asn	Met	Asp	Thr	Ser	Leu	His	Ala	Lys	Val	Gln	His	Leu	Glu	Gly	Val	
465					470				475					480		
Ile	Tyr	Glu														

<210> 355
 <211> 1630
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (294)...(1577)

<400> 355
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 ttgggttagt ctataagact cccatttcaa gctctcctat ctcttatgat ccctacacta 180
 cccccattgg gagcttgtat gctgaaaaat taaaagaaaa ccctaaccat agcgcgggcca 240
 ttcttttaga agatggcttt gacgctctgt tgcataagagt gggacttatt aga atg 296
 Met
 1
 agc caa aaa agc att gac atg caa act tat atc tat aaa aac gac ctt 344
 Ser Gln Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu
 5 10 15

tct tct caa gtg att gct aaa gaa ctt tta aat gcg gcc aat cgt ggg	392
Ser Ser Gln Val Ile Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg Gly	
20 25 30	
gta aaa gtg cgc atc ctt tta gac gat aac gga ttg gat tcg gat ttt	440
Val Lys Val Arg Ile Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp Phe	
35 40 45	
tca gat att atg ctc tta aat ttc cat aaa aac att gag gtg aaa att	488
Ser Asp Ile Met Leu Leu Asn Phe His Lys Asn Ile Glu Val Lys Ile	
50 55 60 65	
ttt aac ccc tac tat atc cgc aat aaa ggc ttg cgt tat ttt gaa atg	536
Phe Asn Pro Tyr Tyr Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu Met	
70 75 80	
ctt gcg gat tat gag cgc att aaa aaa cgc atg cac aac aag ctt ttc	584
Leu Ala Asp Tyr Glu Arg Ile Lys Lys Arg Met His Asn Lys Leu Phe	
85 90 95	
atc gtg gat aat ttc gct gtc att ata ggg ggg cgc aat att ggg gac	632
Ile Val Asp Asn Phe Ala Val Ile Ile Gly Gly Arg Asn Ile Gly Asp	
100 105 110	
aat tat ttt gat aac gat tta gac acg aat ttt tta gat tta gac gct	680
Asn Tyr Phe Asp Asn Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp Ala	
115 120 125	
ttg ttt ttt ggg ggg gtt gct tca aaa gcc aaa gaa agc ttt gaa cgc	728
Leu Phe Phe Gly Gly Val Ala Ser Lys Ala Lys Glu Ser Phe Glu Arg	
130 135 140 145	
tat tgg aga ttc cac cgc tct atc cct gtt tca tta cta aga acc cat	776
Tyr Trp Arg Phe His Arg Ser Ile Pro Val Ser Leu Leu Arg Thr His	
150 155 160	
aaa aga ctc aaa aac aac gct aaa gaa atc gct aaa ctc cat gaa aaa	824
Lys Arg Leu Lys Asn Asn Ala Lys Glu Ile Ala Lys Leu His Glu Lys	
165 170 175	
atc cct atc agc gct gaa gac aaa aac cag ttt gaa aaa aaa gtc aat	872
Ile Pro Ile Ser Ala Glu Asp Lys Asn Gln Phe Glu Lys Lys Val Asn	
180 185 190	
gat ttt ata gat cgt ttc caa aaa tac caa tac ccc att tat tat ggg	920
Asp Phe Ile Asp Arg Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr Gly	
195 200 205	
aat gcc att ttt tta gcc gat tca ccc aaa aaa att gac acg ccc ttg	968
Asn Ala Ile Phe Leu Ala Asp Ser Pro Lys Lys Ile Asp Thr Pro Leu	
210 215 220 225	
tat tcg cct atc aaa atc gct ttt gag aaa gcc ctt aaa aac gct aag	1016
Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys	

230	235	240	
gac tcc gtt ttt atc gct tca tcg tat ttt att cca ggc aaa aag atg			1064
Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Met			
245	250	255	
atg aaa atc ttt aaa aat caa att tct aag ggg att gaa ttg aac atc			1112
Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile			
260	265	270	
ctt acc aat tcc ctt tca tct act gat gcg ata gtg gtc tat ggg gca			1160
Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala			
275	280	285	
tgg gaa agg tat cgc aac caa tta gtg cga atg ggc gcg aat gtc tat			1208
Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val Tyr			
290	295	300	305
gaa ata cga aac gat ttt ttc aac cgc cag att aaa ggg cgc ttt agc			1256
Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser			
310	315	320	
acc aaa cat tcc ttg cat ggc aag acg att gtt ttt gat gac aat tta			1304
Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn Leu			
325	330	335	
acg ctt cta ggg agt ttc aat att gat ccg cgc tct gca tac atc aac			1352
Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn			
340	345	350	
act gaa agc gcg gtt ttg ttt gac aac ccg tct ttt gct aaa agg gtg			1400
Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val			
355	360	365	
cgt ttg tcg ctt aaa gat cat gcc caa caa tca tgg cat ttg gtg gtg			1448
Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val Val			
370	375	380	385
tat cgg cat aga gtg att tgg gaa gcg gtg gaa gaa ggc att tta atc			1496
Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu Ile			
390	395	400	
cat gaa aaa act tcg cct gac act tcc ttc ttt ttg cgc ttg att aaa			1544
His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys			
405	410	415	
gaa tgg tct aaa gtc ctt cct gaa aga gag ctt taaaactttt aatgcgcttt			1597
Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu			
420	425		
atattgcgaa aaagcgatgt tattggtaac ggc			1630
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<400> 356

-443-

Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu
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 <213> Helicobacter pylori

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 ttaaaaaaag gacttttg atg aaa aca ttt gaa att cta aaa cat ttg caa 111
 Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln
 1 5 10
 gcg gat gcg atc gtg tta ttt atg aaa gtg cat aac ttc cat tgg aat 159
 Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn
 15 20 25
 gtg aaa ggc acc gat ttt ttc aat gtg cat aaa gcc act gaa gaa att 207
 Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile
 30 35 40
 tat gaa gag ttt gcg gac atg ttt gac gat ctc gct gaa agg atc gtt 255
 Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val
 45 50 55
 caa tta ggg cat cac ccc tta gtc act tta tcc gaa gcg atc aaa ctc 303
 Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu
 60 65 70 75
 act cgt gtt aaa gaa gaa act aaa acg agc ttc cac tct aaa gac atc 351
 Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile
 80 85 90
 ttt aaa gaa att cta gag gac tac aaa tat cta gaa aaa gaa ttt aaa 399
 Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys
 95 100 105
 gag ctc tct aac acc gct gaa aaa gaa ggc gat aaa gtt acc gta act 447
 Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr
 110 115 120
 tat gcg gat gat caa tta gcc aag ttg caa aaa tcc att tgg atg ctg 495
 Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu
 125 130 135
 caa gcc cat ttg gct taagcgacca aaaagaagcc agcatgagag attacagcga 550
 Gln Ala His Leu Ala
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 <212> PRT
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 35 40 45
 Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His
 50 55 60
 Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu
 65 70 75 80
 Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu
 85 90 95
 Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr
 100 105 110
 Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln
 115 120 125
 Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala
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 Leu Gly
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 Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe
 5 10 15
 tct ata ggt ttt ggc ggg gtt ggc ggg gtt ggc gga gtt ggg ggt gtg 152
 Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val
 20 25 30
 gga ggc gtt gga ggt ttt tgg ggg cca gcc agc gtg ggt tta gga gcg 200
 Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala
 35 40 45 50
 ccc tgg gtg ttt tta ctg gga tct tgc gaa tgg cct ctt ttt aaa acc 248
 Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr

55 60 65
 aat aaa ttt tca gga ttt aat tta aca agc ttg ggt ttt gaa gga aaa 296
 Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys
 70 75 80
 aaa tct tct ctg tgt tca aat aaa aaa taaatcaacc agtgtaacaa 343
 Lys Ser Ser Leu Cys Ser Asn Lys Lys
 85 90
 tacagacaga atgagagaaa agaaaaaatt cct 376
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 <211> 91
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 <213> Helicobacter pylori
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 Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly
 20 25 30
 Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu
 35 40 45
 Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe
 50 55 60
 Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu
 65 70 75 80
 Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys
 85 90
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 agaaagggtta tcacaatgaa tggttatttg agagtaaaaa cctcttattt tttagcgttg 120
 aacgctttga cttttttgtc ttttaactct ttggtgggcg cgaaagaaca gcatcacact 180
 ttgcaaaaag tgacaaccac tgagcaaaaa ttcaatccaa gcgcgcccgt ttcattggcaa 240
 agcgaagaga tgcgtaattc cacaagctct cgcacgggtga tttccaacaa ggaactcaaa 300
 aaaacgggga atttgaatat tgaaaacgcc ttgcaaaacg tgccagggat tcaaatacaga 360
 gacgctacag gcacaggcgt gctgcctaaa atttcggtgc tcaaaatttta agttaatttt 420
 aataattatt tttatagtat gcatcgggttt gaattaa atg aga aag gtt atc aca 475
 Met Arg Lys Val Ile Thr
 1 5
 atg aat ggt tat ttg aga gta aaa acc tct tat ttt tta gcg ttg aac 523
 Met Asn Gly Tyr Leu Arg Val Lys Thr Ser Tyr Phe Leu Ala Leu Asn

10	15	20	
gct ttg act ttt ttg tct ttt aac tct ttg gtg ggc gcg aaa gaa cag	571		
Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu Val Gly Ala Lys Glu Gln			
25 30 35			
cat cac act ttg caa aaa gtg aca acc act gag caa aaa ttc aat cca	619		
His His Thr Leu Gln Lys Val Thr Thr Thr Glu Gln Lys Phe Asn Pro			
40 45 50			
agc gcg ccg ctt tca tgg caa agc gaa gag atg cgt aat tcc aca agc	667		
Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu Met Arg Asn Ser Thr Ser			
55 60 65 70			
tct cgc acg gtg att tcc aac aag gaa ctc aaa aaa acg ggg aat ttg	715		
Ser Arg Thr Val Ile Ser Asn Lys Glu Leu Lys Lys Thr Gly Asn Leu			
75 80 85			
aat att gaa aac gcc ttg caa aac gtg cca ggg att caa atc aga gac	763		
Asn Ile Glu Asn Ala Leu Gln Asn Val Pro Gly Ile Gln Ile Arg Asp			
90 95 100			
gct aca ggc aca ggc gtg ctg cct aaa att tcg gtg cgc ggt ttt ggt	811		
Ala Thr Gly Thr Gly Val Leu Pro Lys Ile Ser Val Arg Gly Phe Gly			
105 110 115			
ggg ggc ggt aac ggg cat agc aat acc aac atg att tta gtc aat ggt	859		
Gly Gly Gly Asn Gly His Ser Asn Thr Asn Met Ile Leu Val Asn Gly			
120 125 130			
atc ccc att tat ggc gcg ccg tat tcc aat att gaa ctg gcg att ttc	907		
Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn Ile Glu Leu Ala Ile Phe			
135 140 145 150			
cct gta act ttc cag tca gtg gat agg att gat gtg att aaa ggg ggc	955		
Pro Val Thr Phe Gln Ser Val Asp Arg Ile Asp Val Ile Lys Gly Gly			
155 160 165			
acg agc gtg caa tac ggc cct aat act ttt gga ggc gtg gtg aat atc	1003		
Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe Gly Gly Val Val Asn Ile			
170 175 180			
atc act aaa gaa atc cct aaa gag tgg gaa aat caa gcg gct gaa agg	1051		
Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu Asn Gln Ala Ala Glu Arg			
185 190 195			
atc act ttt tgg ggg cga tcc tct aat ggg aat ttt gta gat ccc aaa	1099		
Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly Asn Phe Val Asp Pro Lys			
200 205 210			
gaa aaa ggc aag cct tta gcc caa act tta gga aac caa atg ctg ttt	1147		
Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu Gly Asn Gln Met Leu Phe			
215 220 225 230			
aac act tac ggg cga acg gct gga atg ttg ggt aag cat gta gga att	1195		

Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu Gly Lys His Val Gly Ile	
235 240 245	
agc gct caa ggc aat tgg att aac ggg caa ggt ttc agg caa aac agc	1243
Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln Gly Phe Arg Gln Asn Ser	
250 255 260	
ccc aca aag gtg caa aac tac ttg ctt gat gcg gtt tat aag att aat	1291
Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp Ala Val Tyr Lys Ile Asn	
265 270 275	
gcg acc aat act ttt aaa gct tat tac caa tat tat caa tac aac tct	1339
Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln Tyr Tyr Gln Tyr Asn Ser	
280 285 290	
tac cat cca ggc act ttg agt gca caa gat tat gct tat aac cgc ttc	1387
Tyr His Pro Gly Thr Leu Ser Ala Gln Asp Tyr Ala Tyr Asn Arg Phe	
295 300 305 310	
att aat gag cgc cct gac aat caa gat gga ggg cga gcc aag cgc ttt	1435
Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly Gly Arg Ala Lys Arg Phe	
315 320 325	
ggg atc gtg tat caa aat tat ttt ggc gat ccg gat agg aaa gtg ggg	1483
Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp Pro Asp Arg Lys Val Gly	
330 335 340	
gga gat ttt aaa ttc act tat ttc acg cat gac atg agt agg gat ttt	1531
Gly Asp Phe Lys Phe Thr Tyr Phe Thr His Asp Met Ser Arg Asp Phe	
345 350 355	
ggg ttt tcc aac caa tac caa agc gtg tat atg agc agt caa aac aag	1579
Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys	
360 365 370	
att tta cct ttt aaa ggc aag gga aaa att agc gcg act aac cct aat	1627
Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn	
375 380 385 390	
tgc ggt ttg tat tct tat agc gac acg aac agc cct tgt tgg caa ttt	1675
Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe	
395 400 405	
ttt gac aat atc cgc cga tcc gtg gtg aat gcc ttt gag cca aaa ctc	1723
Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu	
410 415 420	
aat ctt atc gtc aat acc ggt aaa gtc aaa caa act ttt aat atg gga	1771
Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly	
425 430 435	
atg cgc ttt tta act gaa gat tta tac cgc cga tcc acc acc agg aaa	1819
Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys	
440 445 450	

aac cct agc atg cct aat aat ggg agt ggt ttt gat gca gga act tca	1867
Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser	
455 460 465 470	
ctc aat aat ttc aac aat tat acc gct gtg tat gcc agc gat gag atc	1915
Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile	
475 480 485	
aat ttc aat aac ggc atg cta acg atc acg ccg ggc ttg aga tac act	1963
Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr	
490 495 500	
ttt tta aat tac gaa aaa aaa gac gct cct cct ttt aaa gca ggc caa	2011
Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Ala Gly Gln	
505 510 515	
aca gga aaa acc att aaa gat cgt tat aac caa tgg aat cca gca gtg	2059
Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn Gln Trp Asn Pro Ala Val	
520 525 530	
aat gtc ggc tat aaa ccc att aaa gaa ttg ttg ttt tat ttc aat tac	2107
Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn Tyr	
535 540 545 550	
caa aga agc tac att ccg cct caa ttc agc aat atc ggt agt ttt gta	2155
Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Ser Phe Val	
555 560 565	
ggc aca agc acg gat tat ttt caa atc ttt aat gtc atg gaa ggc ggc	2203
Gly Thr Ser Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly Gly	
570 575 580	
tca aga tat tat ttt aac aac caa gtg agt ttt aac gcg aat tat ttt	2251
Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser Phe Asn Ala Asn Tyr Phe	
585 590 595	
gtg att ttt gcg aat aac tat ttt acc ggg cgc tat ggg gat aat aaa	2299
Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly Arg Tyr Gly Asp Asn Lys	
600 605 610	
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Glu Pro Val Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr	
615 620 625 630	
acg ccg att aga ggg ctt aat ttc cat gcg gct tac act ttc ata gat	2395
Thr Pro Ile Arg Gly Leu Asn Phe His Ala Ala Tyr Thr Phe Ile Asp	
635 640 645	
gcc aat atc aca agc cac acg atg gtt act aac ccc gct aat cct aaa	2443
Ala Asn Ile Thr Ser His Thr Met Val Thr Asn Pro Ala Asn Pro Lys	
650 655 660	
ggg cct aaa aaa gat att ttt ggc aaa aag ctc cct ttt gta agc ccg	2491
Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys Leu Pro Phe Val Ser Pro	
665 670 675	

cac caa ttc att tta gac gcg agc tac act tac gct aaa acc acg att 2539
 His Gln Phe Ile Leu Asp Ala Ser Tyr Thr Tyr Ala Lys Thr Thr Ile
 680 685 690

ggg ttg agt tct ttc ttt tat agc cga act tat agc gat gtg tta aac 2587
 Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr Tyr Ser Asp Val Leu Asn
 695 700 705 710

acc gtg cct ttt att caa tac gcg ccc acg atc aaa aat ggt gct atc 2635
 Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr Ile Lys Asn Gly Ala Ile
 715 720 725

act acc aaa aca gcg ggc atg acg cca tgg tat tgg gtg tgg aat ttg 2683
 Thr Thr Lys Thr Ala Gly Met Thr Pro Trp Tyr Trp Val Trp Asn Leu
 730 735 740

caa att tct acc act ttt tgg gaa cgc aaa aag caa agc gtt aat gcg 2731
 Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys Lys Gln Ser Val Asn Ala
 745 750 755

agc ttg caa atc aat aac att ttt aac atg aaa tat tgg ttt agc ggg 2779
 Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser Gly
 760 765 770

ata ggc act agc cta acg gga aag aag ccg cgc ctc cta gga gca tca 2827
 Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro Arg Leu Leu Gly Ala Ser
 775 780 785 790

cag cgt atg tgagctatca tttttaattt taggggttgta atgttttgag 2876
 Gln Arg Met

aagttgggcg taaa 2890

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 Val Gly Ala Lys Glu Gln His His Thr Leu Gln Lys Val Thr Thr Thr
 35 40 45
 Glu Gln Lys Phe Asn Pro Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu
 50 55 60
 Met Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu
 65 70 75 80
 Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro
 85 90 95
 Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile
 100 105 110

Ser	Val	Arg	Gly	Phe	Gly	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	
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Met	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	
		130					135				140					
Ile	Glu	Leu	Ala	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	
145					150					155					160	
Asp	Val	Ile	Lys	Gly	Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	
				165					170					175		
Gly	Gly	Val	Val	Asn	Ile	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	
			180					185					190			
Asn	Gln	Ala	Ala	Glu	Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	
		195					200					205				
Asn	Phe	Val	Asp	Pro	Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	
		210				215					220					
Gly	Asn	Gln	Met	Leu	Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	
225					230					235					240	
Gly	Lys	His	Val	Gly	Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	
				245					250					255		
Gly	Phe	Arg	Gln	Asn	Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	
			260					265					270			
Ala	Val	Tyr	Lys	Ile	Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln	
		275					280					285				
Tyr	Tyr	Gln	Tyr	Asn	Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp	
		290				295					300					
Tyr	Ala	Tyr	Asn	Arg	Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly	
305					310					315					320	
Gly	Arg	Ala	Lys	Arg	Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp	
				325					330					335		
Pro	Asp	Arg	Lys	Val	Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His	
			340					345					350			
Asp	Met	Ser	Arg	Asp	Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr	
		355					360					365				
Met	Ser	Ser	Gln	Asn	Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Lys	Ile	
		370				375					380					
Ser	Ala	Thr	Asn	Pro	Asn	Cys	Gly	Leu	Tyr	Ser	Tyr	Ser	Asp	Thr	Asn	
385					390					395					400	
Ser	Pro	Cys	Trp	Gln	Phe	Phe	Asp	Asn	Ile	Arg	Arg	Ser	Val	Val	Asn	
				405					410					415		
Ala	Phe	Glu	Pro	Lys	Leu	Asn	Leu	Ile	Val	Asn	Thr	Gly	Lys	Val	Lys	
			420					425					430			
Gln	Thr	Phe	Asn	Met	Gly	Met	Arg	Phe	Leu	Thr	Glu	Asp	Leu	Tyr	Arg	
		435					440					445				
Arg	Ser	Thr	Thr	Arg	Lys	Asn	Pro	Ser	Met	Pro	Asn	Asn	Gly	Ser	Gly	
		450				455					460					
Phe	Asp	Ala	Gly	Thr	Ser	Leu	Asn	Asn	Phe	Asn	Asn	Tyr	Thr	Ala	Val	
465					470					475					480	
Tyr	Ala	Ser	Asp	Glu	Ile	Asn	Phe	Asn	Asn	Gly	Met	Leu	Thr	Ile	Thr	
			485						490					495		
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Glu	Lys	Lys	Asp	Ala	Pro	
			500					505					510			
Pro	Phe	Lys	Ala	Gly	Gln	Thr	Gly	Lys	Thr	Ile	Lys	Asp	Arg	Tyr	Asn	
		515					520					525				
Gln	Trp	Asn	Pro	Ala	Val	Asn	Val	Gly	Tyr	Lys	Pro	Ile	Lys	Glu	Leu	
		530				535					540					
Leu	Phe	Tyr	Phe	Asn	Tyr	Gln	Arg	Ser	Tyr	Ile	Pro	Pro	Gln	Phe	Ser	

545		550		555		560									
Asn	Ile	Gly	Ser	Phe	Val	Gly	Thr	Ser	Thr	Asp	Tyr	Phe	Gln	Ile	Phe
				565					570					575	
Asn	Val	Met	Glu	Gly	Gly	Ser	Arg	Tyr	Tyr	Phe	Asn	Asn	Gln	Val	Ser
			580					585					590		
Phe	Asn	Ala	Asn	Tyr	Phe	Val	Ile	Phe	Ala	Asn	Asn	Tyr	Phe	Thr	Gly
		595					600					605			
Arg	Tyr	Gly	Asp	Asn	Lys	Glu	Pro	Val	Asn	Ala	Arg	Ser	Gln	Gly	Val
	610					615					620				
Glu	Leu	Glu	Leu	Tyr	Tyr	Thr	Pro	Ile	Arg	Gly	Leu	Asn	Phe	His	Ala
	625					630				635					640
Ala	Tyr	Thr	Phe	Ile	Asp	Ala	Asn	Ile	Thr	Ser	His	Thr	Met	Val	Thr
			645						650					655	
Asn	Pro	Ala	Asn	Pro	Lys	Gly	Pro	Lys	Lys	Asp	Ile	Phe	Gly	Lys	Lys
		660						665					670		
Leu	Pro	Phe	Val	Ser	Pro	His	Gln	Phe	Ile	Leu	Asp	Ala	Ser	Tyr	Thr
	675						680					685			
Tyr	Ala	Lys	Thr	Thr	Ile	Gly	Leu	Ser	Ser	Phe	Phe	Tyr	Ser	Arg	Thr
	690					695					700				
Tyr	Ser	Asp	Val	Leu	Asn	Thr	Val	Pro	Phe	Ile	Gln	Tyr	Ala	Pro	Thr
	705				710				715					720	
Ile	Lys	Asn	Gly	Ala	Ile	Thr	Thr	Lys	Thr	Ala	Gly	Met	Thr	Pro	Trp
			725					730						735	
Tyr	Trp	Val	Trp	Asn	Leu	Gln	Ile	Ser	Thr	Thr	Phe	Trp	Glu	Arg	Lys
		740					745						750		
Lys	Gln	Ser	Val	Asn	Ala	Ser	Leu	Gln	Ile	Asn	Asn	Ile	Phe	Asn	Met
	755					760						765			
Lys	Tyr	Trp	Phe	Ser	Gly	Ile	Gly	Thr	Ser	Leu	Thr	Gly	Lys	Lys	Pro
	770				775						780				
Arg	Leu	Leu	Gly	Ala	Ser	Gln	Arg	Met							
785					790										

<210> 363
 <211> 406
 <212> DNA
 <213> Helicobacter pylori

<220>
 <221> CDS
 <222> (51)...(353)

<400> 363	
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	Ile Lys
	1
ata atc tat caa atc atc aag ttt ttt cgt tct aag aat ttt att ttg	104
Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe Ile Leu	
	5 10 15
ttt ttt aga ata gca acg ata aag ttc ttc ttt tat ctc att tgg gaa	152
Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile Trp Glu	
	20 25 30

ttt ttg aat gtt ata gac aat ttc act atc tct ttg att ttg ttt ata 200
Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile
35 40 45 50

ttt ttt agc ccc ata cca aag aaa tat ttg ata aaa aat aag aaa aat 248
Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn
55 60 65

agc gta aaa gaa aaa gaa aat aaa gaa aaa aga aag aga aaa aga aag 296
Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys
70 75 80

gat ttt gtt ttg ggt gta ttg gaa aat aga ctc aaa aat caa ttg aaa 344
Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys
85 90 95

aac ccc ttt tagattaaaa ataaaaacaa taagcgaaac gacaaaagca 393
Asn Pro Phe
100

agcagaaaag aag 406

<210> 364
<211> 101
<212> PRT
<213> Helicobacter pylori

<400> 364
Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe
1 5 10 15
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile
20 25 30
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu
35 40 45
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys
50 55 60
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys
65 70 75 80
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln
85 90 95
Leu Lys Asn Pro Phe
100

<210> 365
<211> 1143
<212> DNA
<213> Helicobacter pylori

<220>
<221> CDS
<222> (89)...(1087)

<400> 365
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ctccataaat catacaaaaa ggatcggtt atg tta gtt act cgc ttt aaa aaa	112
Met Leu Val Thr Arg Phe Lys Lys	
1 5	
gct tta atc tct tat tct tta ggc gcg ctt ctt gtt tca tcg tta ttg	160
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu	
10 15 20	
ggc gtg gct agt gct tcc aat caa gaa atc caa gtc aaa gat tat ttt	208
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe	
25 30 35 40	
ggg gat caa gcc atc aag ctt cct gtt tct aaa ata atc tac ttg ggt	256
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly	
45 50 55	
agc ttt gca gaa gtg cct gct atg ttc cat act tgg gat agg gtc gtg	304
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val	
60 65 70	
gga att tcg gat tac gct ttt aaa tct gat att gtt aaa gct act ctc	352
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu	
75 80 85	
aaa gat cct aaa cgc att aaa tcc atg agc agt gat cat gtg gcg gcg	400
Lys Asp Pro Lys Arg Ile Lys Ser Met Ser Ser Asp His Val Ala Ala	
90 95 100	
ttg aat gtg gag ctt tta aaa aag ctt ggc ccc gat ctt gtg gta acc	448
Leu Asn Val Glu Leu Leu Lys Lys Leu Gly Pro Asp Leu Val Val Thr	
105 110 115 120	
ttt gtg ggc aac cct aaa gcg gta gag cat gcg aaa aaa ttt ggt ata	496
Phe Val Gly Asn Pro Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile	
125 130 135	
tta ttt ctt tct ttc caa gaa aaa acc att gca gaa gtc atg gaa gat	544
Leu Phe Leu Ser Phe Gln Glu Lys Thr Ile Ala Glu Val Met Glu Asp	
140 145 150	
att gac gct caa gct aaa gcc tta gaa att gat gct tct aaa aaa ctg	592
Ile Asp Ala Gln Ala Lys Ala Leu Glu Ile Asp Ala Ser Lys Lys Leu	
155 160 165	
gcc aaa atg caa gaa act ttg gat ttt att gct gag cgt ttg aaa ggt	640
Ala Lys Met Gln Glu Thr Leu Asp Phe Ile Ala Glu Arg Leu Lys Gly	
170 175 180	
gtc aaa aag aaa aaa ggg gtg gag ctt ttc cat aag gcc aat aag atc	688
Val Lys Lys Lys Lys Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile	
185 190 195 200	
agc ggc cat caa gcc ctt gat tca gac att tta gaa aaa gga ggc ata	736
Ser Gly His Gln Ala Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile	
205 210 215	

gac aat ttt ggc ttg aaa tat gtc aaa ttt ggg cgt gct gac att agc 784
Asp Asn Phe Gly Leu Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser
220 225 230

gtg gaa aaa atc gtt aaa gaa aac cct gag att atc ttt att tgg tgg 832
Val Glu Lys Ile Val Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp
235 240 245

ata agc cca ctc acg cct gaa gat gtg tta aac aac ccc aaa ttt gct 880
Ile Ser Pro Leu Thr Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ala
250 255 260

acc atc aaa gcc att aaa aac aag cag gtt tat aaa ctc ccc aca atg 928
Thr Ile Lys Ala Ile Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met
265 270 275 280

gat att ggc ggg cct aga gcc cca ctc ata agt ctt ttt atc gct cta 976
Asp Ile Gly Gly Pro Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu
285 290 295

aaa gcc cac cct gaa gcc ttt aag ggc gtg gat att aat gcg att gtt 1024
Lys Ala His Pro Glu Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Val
300 305 310

aaa gac tac tat aaa gtg gtt ttt gat ttg aat gat gca gag gtt gaa 1072
Lys Asp Tyr Tyr Lys Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu
315 320 325

ccc ttt tta tgg cat taatttttaa aaaagggctg atatttttag ccctttgtgt 1127
Pro Phe Leu Trp His
330

atcgcgctag gattag 1143

<210> 366
<211> 333
<212> PRT
<213> Helicobacter pylori

<400> 366
Met Leu Val Thr Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
1 5 10 15
Ala Leu Leu Val Ser Ser Leu Leu Gly Val Ala Ser Ala Ser Asn Gln
20 25 30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Asp Gln Ala Ile Lys Leu Pro
35 40 45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
50 55 60
Phe His Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
65 70 75 80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Lys Arg Ile Lys Ser
85 90 95
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys
100 105 110

Leu Gly Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val
 115 120 125
 Glu His Ala Lys Lys Phe Gly Ile Leu Phe Leu Ser Phe Gln Glu Lys
 130 135 140
 Thr Ile Ala Glu Val Met Glu Asp Ile Asp Ala Gln Ala Lys Ala Leu
 145 150 155 160
 Glu Ile Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu Thr Leu Asp
 165 170 175
 Phe Ile Ala Glu Arg Leu Lys Gly Val Lys Lys Lys Lys Gly Val Glu
 180 185 190
 Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Leu Asp Ser
 195 200 205
 Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val
 210 215 220
 Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn
 225 230 235 240
 Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp
 245 250 255
 Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys
 260 265 270
 Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro
 275 280 285
 Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys
 290 295 300
 Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val Val Phe
 305 310 315 320
 Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
 325 330

<210> 367
 <211> 898
 <212> DNA
 <213> *Helicobacter pylori*

<220>
 <221> CDS
 <222> (51)...(845)

<400> 367
 gggggggttat agtaaaaaca tgcaagtaat ttaaagttaa ttttaagataa tta ggc 56
 Leu Gly
 1

 aca ata gcc aca aaa agt tta agg ctg tat ttg aaa act cta ttt agt 104
 Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu Phe Ser
 5 10 15

 att tat ctc ttt tta tcg ttg aac cca ctc ttt tta gaa gct aat gaa 152
 Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala Asn Glu
 20 25 30

 atc act tgg tct aaa ttc ttg gaa aat ttt aaa aac aag aat gat gat 200
 Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn Asp Asp
 35 40 45 50

gac aaa cct aaa ccc cta act att gat aaa aac aat gaa aaa cag caa	248
Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln	
55 60 65	
atc tta gac aaa aac cag caa atc tta aaa agg gct ttg gaa aaa agc	296
Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser	
70 75 80	
ctt aaa ttc ttt ttc att ttt gga tac aac tat tcg caa gcc act ttt	344
Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe	
85 90 95	
tca act tct aac caa acc ttg act ttt gta gcc aat agc ata ggg ttt	392
Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe	
100 105 110	
aac acc gct acc ggt tta gag cat ttt tta aga aac cac cct aaa gtc	440
Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val	
115 120 125 130	
ggt ttt aga atc ttt agc gtc tat aac tat ttc cat tct gtt tcc ctc	488
Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu	
135 140 145	
tcc cag cct caa acc tta atg gtg caa aat tat ggg ggc gcg tta gat	536
Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp	
150 155 160	
ttt tct tgg att ttt gta gat aaa aat att tat cgc ttt agg agt tat	584
Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr	
165 170 175	
tta ggg atc gct tta gaa caa ggg gtg ttg tta gtg gat acg att aaa	632
Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys	
180 185 190	
cca ggt gct atc aca acg att atc cca aga acc aaa aaa acc ttt ttt	680
Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe	
195 200 205 210	
caa gcc cct ttg cgt ttt ggt ttt atc gtg gat ttt atc ggc tat ttg	728
Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu	
215 220 225	
tct ttg caa tta ggg att gaa atg cct tta gtg agg aat gtt ttt tac	776
Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr	
230 235 240	
acc tac aac aac cat caa gaa aga ttc aaa cca cga ttt aac gct aat	824
Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn	
245 250 255	
ctt tct tta atc gtt tcg ttt tagccccct tttccccctt taaataagcc	875
Leu Ser Leu Ile Val Ser Phe	

260

265

catgattttc ctagggtatt tta

898

<210> 368

<211> 265

<212> PRT

<213> Helicobacter pylori

<400> 368

Leu	Gly	Thr	Ile	Ala	Thr	Lys	Ser	Leu	Arg	Leu	Tyr	Leu	Lys	Thr	Leu
1				5					10					15	
Phe	Ser	Ile	Tyr	Leu	Phe	Leu	Ser	Leu	Asn	Pro	Leu	Phe	Leu	Glu	Ala
		20						25					30		
Asn	Glu	Ile	Thr	Trp	Ser	Lys	Phe	Leu	Glu	Asn	Phe	Lys	Asn	Lys	Asn
		35					40					45			
Asp	Asp	Asp	Lys	Pro	Lys	Pro	Leu	Thr	Ile	Asp	Lys	Asn	Asn	Glu	Lys
	50					55					60				
Gln	Gln	Ile	Leu	Asp	Lys	Asn	Gln	Gln	Ile	Leu	Lys	Arg	Ala	Leu	Glu
65					70					75				80	
Lys	Ser	Leu	Lys	Phe	Phe	Phe	Ile	Phe	Gly	Tyr	Asn	Tyr	Ser	Gln	Ala
				85					90					95	
Thr	Phe	Ser	Thr	Ser	Asn	Gln	Thr	Leu	Thr	Phe	Val	Ala	Asn	Ser	Ile
			100					105						110	
Gly	Phe	Asn	Thr	Ala	Thr	Gly	Leu	Glu	His	Phe	Leu	Arg	Asn	His	Pro
		115				120						125			
Lys	Val	Gly	Phe	Arg	Ile	Phe	Ser	Val	Tyr	Asn	Tyr	Phe	His	Ser	Val
	130					135					140				
Ser	Leu	Ser	Gln	Pro	Gln	Thr	Leu	Met	Val	Gln	Asn	Tyr	Gly	Gly	Ala
145					150					155					160
Leu	Asp	Phe	Ser	Trp	Ile	Phe	Val	Asp	Lys	Asn	Ile	Tyr	Arg	Phe	Arg
			165						170					175	
Ser	Tyr	Leu	Gly	Ile	Ala	Leu	Glu	Gln	Gly	Val	Leu	Leu	Val	Asp	Thr
		180						185					190		
Ile	Lys	Pro	Gly	Ala	Ile	Thr	Thr	Ile	Ile	Pro	Arg	Thr	Lys	Lys	Thr
		195					200						205		
Phe	Phe	Gln	Ala	Pro	Leu	Arg	Phe	Gly	Phe	Ile	Val	Asp	Phe	Ile	Gly
	210					215					220				
Tyr	Leu	Ser	Leu	Gln	Leu	Gly	Ile	Glu	Met	Pro	Leu	Val	Arg	Asn	Val
225					230					235				240	
Phe	Tyr	Thr	Tyr	Asn	Asn	His	Gln	Glu	Arg	Phe	Lys	Pro	Arg	Phe	Asn
				245					250					255	
Ala	Asn	Leu	Ser	Leu	Ile	Val	Ser	Phe							
		260						265							

<210> 369

<211> 742

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51) ... (689)

<400> 369

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Lys Lys	
1	
cag tta aaa aat tgc gtt aag cta aaa cta ttt tta agg aaa aat ttg	104
Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu	
5 10 15	
gat att tta gat ttg aac aaa gcg caa gcg gtg caa caa aat gaa caa	152
Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln	
20 25 30	
gag gta gag gat aaa gag cga gag tct aaa gag ccg gtg gtt tta gaa	200
Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu	
35 40 45 50	
gat ttg agc gct tta gcg tgg ctt gaa tta gaa gag ttt agc cgc ctt	248
Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu	
55 60 65	
tca ggg ctt cct aaa gaa agg att ttg gaa tta gtg aat ctt ggt aaa	296
Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys	
70 75 80	
atc aag agc aaa ata agc agc aac aag ctt tta att gat gcg agc agc	344
Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser	
85 90 95	
ggg aca aac gct tta atc aaa aag gta gaa aat agt ttg att tct atg	392
Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met	
100 105 110	
gat atg aac ggg cgt tct tta gaa cct gtg ttt gtg gaa aag acc att	440
Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile	
115 120 125 130	
aac acg att tta aac ttg cat gat aag gtc att ggc gct aaa gat gaa	488
Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu	
135 140 145	
acg att tca gcc ttt aaa aat gaa aac atg ttt tta aaa gac gct tta	536
Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu	
150 155 160	
atc tct atg caa gaa gtc tat gaa gaa gat aaa aaa acc att gat ctt	584
Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu	
165 170 175	
ttg cgc gat gaa ctc aat caa gcg aga gaa gaa att gaa ttt atg aag	632
Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys	
180 185 190	
agg aaa tac cgc ttg atg tgg ggg aaa gtc gct gac atg agc agc gtg	680
Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val	

195

200

205

210

aat aaa aag tagttttaaa ttaacgcca tgctgagggc ttattagcgg
Asn Lys Lys

729

taatttttagg tga

742

<210> 370

<211> 213

<212> PRT

<213> Helicobacter pylori

<400> 370

Lys Lys Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys
1 5 10 15
Asn Leu Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn
20 25 30
Glu Gln Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val
35 40 45
Leu Glu Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser
50 55 60
Arg Leu Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu
65 70 75 80
Gly Lys Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala
85 90 95
Ser Ser Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile
100 105 110
Ser Met Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys
115 120 125
Thr Ile Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys
130 135 140
Asp Glu Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp
145 150 155 160
Ala Leu Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile
165 170 175
Asp Leu Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe
180 185 190
Met Lys Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser
195 200 205
Ser Val Asn Lys Lys
210